

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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This application is a continuation-in-part of the following applications:

10 (1) provisional application Ser. No. 60/096,622 (GI 6075), filed August 14, 1998;
(2) provisional application Ser. No. 60/096,815 (GI 6076), filed August 17, 1998;
(3) provisional application Ser. No. 60/099,229 (GI 6077), filed September 4, 1998;
(4) provisional application Ser. No. 60/105,368 (GI 6078), filed October 23, 1998;
(5) provisional application Ser. No. 60/115,234 (GI 6079), filed January 8, 1999;
(6) provisional application Ser. No. 60/119,931 (GI 6080), filed February 12, 1999;
(7) provisional application Ser. No. 60/120,575 (GI 6081), filed February 18, 1999;
15 (8) provisional application Ser. No. 60/132,020 (GI 6082), filed April 30, 1999;
(9) provisional application Ser. No. 60/XXXX,XXX (GI 6083), filed August 11, 1999;
all of which are incorporated by reference herein.

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

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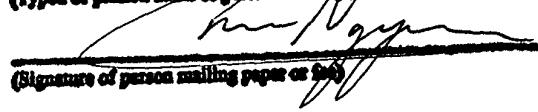
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BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the 5 past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which 10 isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the 15 cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an 20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co62_12 deposited under accession 25 number ATCC 98825;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co62_12 deposited under accession number ATCC 98825;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:1.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821; the nucleotide sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821; the nucleotide sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625; the nucleotide sequence of the full-length protein coding sequence of clone co62_12 deposited under accession number ATCC 98825; or the

25 nucleotide sequence of a mature protein coding sequence of clone co62_12 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having

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biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
- (ab) the nucleotide sequence of the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 25 (ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
- (bb) the nucleotide sequence of the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 30 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to

a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821, and extending

5 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 87 to nucleotide 821. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

10 NO:1 from nucleotide 120 to nucleotide 821, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 120 to nucleotide 821. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

15 corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 1 to nucleotide 1625.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the

25 fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone co62_12 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred

30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013;

10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825;

15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825;

20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013; the nucleotide sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013; the nucleotide sequence of the full-length protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825; or the

5 nucleotide sequence of a mature protein coding sequence of clone lo311_8 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

10 comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 162

15 to amino acid 171 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

20 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the

25 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

30 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

5 (bb) the nucleotide sequence of the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

10 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to 15 a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of 20 SEQ ID NO:3 from nucleotide 9 to nucleotide 1013, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 9 to nucleotide 1013. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013, and extending contiguously from a 25 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 96 to nucleotide 1013.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 30 consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone lo311_8 deposited under accession number ATCC 98825; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from 10 amino acid 162 to amino acid 171 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825; the nucleotide sequence of the full-length 10 protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone ns197_1 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert 15 of clone ns197_1 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological 20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced 25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in 15 conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending 20 contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825, and extending 25 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 352 to nucleotide 825.

In other embodiments, the present invention provides a composition comprising 30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone ns197_1 deposited under accession number ATCC 98825; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred 5. embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from 10. amino acid 74 to amino acid 83 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829;
- 20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829; the nucleotide sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829; the nucleotide sequence of the full-length protein coding sequence of clone pj193_5 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone pj193_5 deposited

15 under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological

20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 119 to amino acid 128 of SEQ ID NO:8.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone
pj193_5 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

5 (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the
3' end of SEQ ID NO:7; and

15 (bb) the nucleotide sequence of the cDNA insert of clone
pj193_5 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending
contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to
a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the
poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated

25 according to the above process comprises a nucleotide sequence corresponding to the
cDNA sequence of SEQ ID NO:7 from nucleotide 86 to nucleotide 829, and extending
contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of
SEQ ID NO:7 from nucleotide 86 to nucleotide 829, to a nucleotide sequence
corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 86 to
30 nucleotide 829. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:7 from nucleotide 149 to nucleotide 829, and extending contiguously from a
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from

nucleotide 149 to nucleotide 829, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 149 to nucleotide 829.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

10 (c) the amino acid sequence encoded by the cDNA insert of clone pj193_5 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably 15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 119 to amino acid 128 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an 20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292;
- 25 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;
- 30 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

10 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:9.

15 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292; the nucleotide sequence of the full-length protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone pj317_2 deposited under accession number ATCC 98825. In other preferred embodiments, the

20 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

25 preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 181 to amino acid 190 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 30 ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 5' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone pj317_2 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated

30 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292, to a nucleotide sequence

corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 174 to nucleotide 1292.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

10 pj317_2 deposited under accession number ATCC 98825;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably 15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 181 to amino acid 190 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an 20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt332_1 deposited under accession 25 number ATCC 98825;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517; the nucleotide sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517; the nucleotide sequence of the full-length protein 20 coding sequence of clone pt332_1 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone pt332_1 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825. In further preferred 25 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having 30 biological activity, the fragment comprising the amino acid sequence from amino acid 413 to amino acid 422 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

5 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide

2517, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 7 to nucleotide 2517. Also preferably the polynucleotide isolated according to the above

5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 904 to nucleotide 2517.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pt332_1 deposited under accession number ATCC 98825;

15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred 20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence 25 from amino acid 413 to amino acid 422 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- 10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 15 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any 20 one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257; the nucleotide sequence of the full-length protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone qc297_15 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein 25 comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having 30

biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and
 - (ab) the nucleotide sequence of the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and
 - (bb) the nucleotide sequence of the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

10 ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 5 257, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 18 to nucleotide 257.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone qc297_15 deposited under accession number ATCC 98825;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 30 NO:15 from nucleotide 21 to nucleotide 2432;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825;

5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

15 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any 20 one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432; the nucleotide sequence of the full-length protein coding sequence of clone qg596_12 deposited under accession number ATCC 25 98825; or the nucleotide sequence of a mature protein coding sequence of clone qg596_12 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825. In further preferred 30 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having

biological activity, the fragment comprising the amino acid sequence from amino acid 397 to amino acid 406 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

15 (ab) the nucleotide sequence of the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

5 ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 21 to nucleotide 2432.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:16;
- (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qg596_12 deposited under accession number ATCC 98825;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 397 to amino acid 406 of SEQ ID NO:16.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105; the nucleotide sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105; the nucleotide sequence of the full-length protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825; or the nucleotide sequence of a mature protein coding sequence of clone rb649_3 deposited under accession number ATCC 98825. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 289 5 to amino acid 298 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 15 3' end of SEQ ID NO:17; and
 - (ab) the nucleotide sequence of the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the 20 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 25 3' end of SEQ ID NO:17; and
 - (bb) the nucleotide sequence of the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii). 30

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 339 to nucleotide 2105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from

15 nucleotide 501 to nucleotide 2105, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 501 to nucleotide 2105.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

20 (a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone rb649_3 deposited under accession number ATCC 98825;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

30 of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 289 to amino acid 298 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467;

5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;

10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;

15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any 25 one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467; the nucleotide sequence of the full-length protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone ca106_19x deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

of clone ca106_19x deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 321 to amino acid 330 of SEQ ID NO:20.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
10 ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
(ab) the nucleotide sequence of the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
(iii) isolating the DNA polynucleotides detected with the probe(s);

25 and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
(bb) the nucleotide sequence of the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 509 to nucleotide 2467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 15 509 to nucleotide 2467.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ca106_19x deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such 25 protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ 30 ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 321 to amino acid 330 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802;

5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835;

10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835;

15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 30 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802; the nucleotide sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802; the nucleotide sequence of the full-length protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835; or the

nucleotide sequence of a mature protein coding sequence of clone ci52_2 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835. In further preferred embodiments, the 5 present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the 10 fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced 15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 20 3' end of SEQ ID NO:21; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ci52_2 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in 25 conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:21, but excluding the poly(A) tail at the 30 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone
ci52_2 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 179 to nucleotide 802. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802, and extending contiguously from a
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 242 to nucleotide 802.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
25 consisting of:

(a) the amino acid sequence of SEQ ID NO:22;
(b) a fragment of the amino acid sequence of SEQ ID NO:22, the
fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
(c) the amino acid sequence encoded by the cDNA insert of clone
30 ci52_2 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:22.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 10 NO:23 from nucleotide 46 to nucleotide 714;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone md124_16 deposited under accession 15 number ATCC 98835;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone md124_16 deposited under accession number 20 ATCC 98835;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of 25 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714; the nucleotide sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714; the nucleotide sequence of the full-length protein coding sequence of clone md124_16 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone md124_16 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 106 to amino acid 115 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

10 (bb) the nucleotide sequence of the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 15 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 20 corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 46 to nucleotide 714. Also preferably the polynucleotide isolated according to the above 25 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 538 to nucleotide 714.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone md124_16 deposited under accession number ATCC 98835;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

10 of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 106 to amino acid 115 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726;

20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835;

25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726; the nucleotide sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726; the nucleotide sequence of the full-length protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pk366_7 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 267 to amino acid 276 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the

30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 92 to nucleotide 1726, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide

92 to nucleotide 1726. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from 5 nucleotide 1211 to nucleotide 1726, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 1211 to nucleotide 1726.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

10 (a) the amino acid sequence of SEQ ID NO:26;
(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
(c) the amino acid sequence encoded by the cDNA insert of clone pk366_7 deposited under accession number ATCC 98835;

15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
20 of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 267 to amino acid 276 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788;
(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788;
30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any 20 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788; the nucleotide sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788; the nucleotide sequence of the full-length protein 25 coding sequence of clone pl741_5 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pl741_5 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835. In further preferred 30 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having

biological activity, the fragment comprising the amino acid sequence from amino acid 290 to amino acid 299 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii):

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 5 1788, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 16 to nucleotide 1788. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID 10 NO:27 from nucleotide 61 to nucleotide 1788, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 61 to nucleotide 1788.

In other embodiments, the present invention provides a composition comprising 15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone pl741_5 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the 25 amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 290 to amino acid 299 of SEQ ID NO:28.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338; the nucleotide sequence of the full-length protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pp314_19 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having 5 biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced 10 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 15 3' end of SEQ ID NO:29; and
 - (ab) the nucleotide sequence of the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in 20 conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:29, but excluding the poly(A) tail at the 25 3' end of SEQ ID NO:29; and
 - (bb) the nucleotide sequence of the cDNA insert of clone pp314_19 deposited under accession number ATCC 98835;
 - (ii) hybridizing said primer(s) to human genomic DNA in 30 conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 5 ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338, and extending contiguously from a nucleotide sequence corresponding to the 5' end 10 of said sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 629 to nucleotide 2338.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 15 consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (c) the amino acid sequence encoded by the cDNA insert of clone 20 pp314_19 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably 25 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an 30 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:31.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102; the nucleotide sequence of the full-length protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pv35_1 deposited under accession number ATCC 98835. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:32.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

15 (ab) the nucleotide sequence of the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but 5 excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102, and extending contiguously from a nucleotide sequence corresponding to the 5' end 10 of said sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 158 to nucleotide 1102.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:32;
- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pv35_1 deposited under accession number ATCC 98835;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 152 to amino acid 161 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:33.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733; the nucleotide sequence of the full-length protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone pw337_6 deposited under accession number ATCC 98835. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:34.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
 - (ab) the nucleotide sequence of the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
 - (bb) the nucleotide sequence of the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 413 to nucleotide 733.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone pw337_6 deposited under accession number ATCC 98835;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:35.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938; the nucleotide sequence of the full-length protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone rd610_1 deposited under accession number ATCC 98835. In other preferred embodiments, the 30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:36.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

10 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

15 (ab) the nucleotide sequence of the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 678 to nucleotide 938.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:36;

(b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone rd610_1 deposited under accession number ATCC 98835;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835;

10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494; the nucleotide sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494; the nucleotide sequence of the full-length protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835; or the nucleotide sequence of a mature protein coding sequence of clone rd810_6 deposited under accession number ATCC 98835. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding 5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 15 consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 30 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and

5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide

10 494, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 75 to nucleotide 494. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

15 NO:37 from nucleotide 447 to nucleotide 494, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 447 to nucleotide 494.

In other embodiments, the present invention provides a composition comprising

20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone rd810_6 deposited under accession number ATCC 98835;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

30 amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 30 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080; the nucleotide sequence of the full-length protein coding sequence of clone cf85_1 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone cf85_1 deposited

under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein 5 comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 10 to amino acid 154 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(aa) SEQ ID NO:39, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:39; and
(ab) the nucleotide sequence of the cDNA insert of clone cf85_1 deposited under accession number ATCC 98850;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(ba) SEQ ID NO:39, but excluding the poly(A) tail at the
3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone
cf85_1 deposited under accession number ATCC 98850;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 181 to nucleotide 1080.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
- (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
- (c) the amino acid sequence encoded by the cDNA insert of clone 25 cf85_1 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348; the nucleotide sequence of SEQ ID NO:41

from nucleotide 599 to nucleotide 1348; the nucleotide sequence of the full-length protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone dd504_18 deposited under accession number ATCC 98850. In other preferred embodiments, the 5 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most 10 preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 15 ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize 20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25 30 and
 - (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 15 corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 161 to nucleotide 1348. Also preferably the polynucleotide isolated according to the above 20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 599 to nucleotide 1348.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the

30 fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone dd504_18 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ 5 ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 10 NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone np26_3 deposited under accession 15 number ATCC 98850;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone np26_3 deposited under accession number 20 ATCC 98850;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of 25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386; the nucleotide sequence of the full-length protein coding sequence of clone np26_3 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone np26_3 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 214 to amino acid 223 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and 15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 20 1386, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 70 to nucleotide 1386.

In other embodiments, the present invention provides a composition comprising 25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone np26_3 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence 5 from amino acid 214 to amino acid 223 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID 5 NO:45 from nucleotide 60 to nucleotide 3515; the nucleotide sequence of the full-length protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone pm412_12 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert 10 of clone pm412_12 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding 15 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 571 to amino acid 580 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

20 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 25 consisting of:
(aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
(ab) the nucleotide sequence of the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;
(ii) hybridizing said probe(s) to human genomic DNA in 30 conditions at least as stringent as 4X SSC at 50 degrees C; and
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and 15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 20 3515, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 60 to nucleotide 3515.

In other embodiments, the present invention provides a composition comprising 25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:46;

(b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone pm412_12 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence 5 from amino acid 571 to amino acid 580 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of 30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780; the nucleotide sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780; the nucleotide sequence of the full-length protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone pm421_3 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and
 - (bb) the nucleotide sequence of the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 1490 to nucleotide 1780. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 1556 to nucleotide 1780.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;

- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pm421_3 deposited under accession number ATCC 98850;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

10 of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486;

20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;

25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;

30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- 5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486; the nucleotide sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486; the nucleotide sequence of the full-length protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone pv6_1 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bb) the nucleotide sequence of the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the

30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 64 to nucleotide 486, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide

64 to nucleotide 486. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from 5 nucleotide 217 to nucleotide 486, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 217 to nucleotide 486.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pv6_1 deposited under accession number ATCC 98850;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783;
- 30 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783; the nucleotide sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783; the nucleotide sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938; the nucleotide sequence of the full-length protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone qs14_3 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino

acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, 5 most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 562 to amino acid 571 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 10 ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:51, but excluding the poly(A) tail at the 15 3' end of SEQ ID NO:51; and
 - (ab) the nucleotide sequence of the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 25 and
 - (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:51, but excluding the poly(A) tail at the 30 3' end of SEQ ID NO:51; and
 - (bb) the nucleotide sequence of the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the

10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 379 to nucleotide 3783, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide

15 379 to nucleotide 3783. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783, to a nucleotide sequence corresponding to the 3' end

20 of said sequence of SEQ ID NO:51 from nucleotide 460 to nucleotide 3783. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938,

25 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 1983 to nucleotide 3938.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:52;

(b) the amino acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135;

(c) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(d) the amino acid sequence encoded by the cDNA insert of clone qs14_3 deposited under accession number ATCC 98850; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52 or the amino acid sequence of SEQ ID NO:52 from amino acid 536 to amino acid 1135. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 562 to amino acid 571 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843; the nucleotide sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843; the nucleotide sequence of the full-length protein coding sequence of clone qy338_9 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone qy338_9 deposited 15 under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qy338_9 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological 20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 135 to amino acid 144 of SEQ ID NO:54.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone
qy338_9 deposited under accession number ATCC 98850;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

5 (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the
3' end of SEQ ID NO:53; and

15 (bb) the nucleotide sequence of the cDNA insert of clone
qy338_9 deposited under accession number ATCC 98850;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the
25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide
843, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:53 from nucleotide 1 to nucleotide 843, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide
30 1 to nucleotide 843. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:53 from nucleotide 469 to nucleotide 843, and extending contiguously from a
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from

nucleotide 469 to nucleotide 843, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 469 to nucleotide 843.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone 10 qy338_9 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably 15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 135 to amino acid 144 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an 20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906; the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906; the nucleotide sequence of the full-length protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850; or the nucleotide sequence of a mature protein coding sequence of clone rc58_1 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
 - (ab) the nucleotide sequence of the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 15 and
 - (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
 - (bb) the nucleotide sequence of the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and 30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide

906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 283 to nucleotide 906. Also preferably the polynucleotide isolated according to the above 5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 906.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the 15 fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rc58_1 deposited under accession number ATCC 98850;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred 20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence 25 from amino acid 99 to amino acid 108 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd232_5 deposited under accession 30 number ATCC 98850;

(d) a polyriuucleotide encoding the full-length protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;

5 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;

10 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

15 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:57.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973; the nucleotide sequence of the full-length protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850;

25 or the nucleotide sequence of a mature protein coding sequence of clone rd232_5 deposited under accession number ATCC 98850. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

30 comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having

biological activity, the fragment comprising the amino acid sequence from amino acid 148 to amino acid 157 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(ab) the nucleotide sequence of the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

5 ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 56 to nucleotide 973.

10 In other embodiments, the present invention provides a composition comprising 10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone rd232_5 deposited under accession number ATCC 98850;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 148 to amino acid 157 of SEQ ID NO:58.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 30 NO:59 from nucleotide 893 to nucleotide 2596;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918;

5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

15 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596; the nucleotide sequence of the full-length protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone ck213_12 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having

biological activity, the fragment comprising the amino acid sequence from amino acid 279 to amino acid 288 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(ab) the nucleotide sequence of the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(bb) the nucleotide sequence of the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 5 2596, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 893 to nucleotide 2596.

In other embodiments, the present invention provides a composition comprising 10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone ck213_12 deposited under accession number ATCC 98918;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the 20 amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 279 to amino acid 288 of SEQ ID NO:60.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 30 NO:61 from nucleotide 29 to nucleotide 1750;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918;

5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

15 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:61.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750; the nucleotide sequence of the full-length protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone pg195_1 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein 25 comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having 30

biological activity, the fragment comprising the amino acid sequence from amino acid 282 to amino acid 291 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

10 ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 5 1750, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 29 to nucleotide 1750.

15 In other embodiments, the present invention provides a composition comprising 10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
- (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone pg195_1 deposited under accession number ATCC 98918;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 282 to amino acid 291 of SEQ ID NO:62.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440; the nucleotide sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440; the nucleotide sequence of the full-length protein coding sequence of clone pw460_5 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone pw460_5

30 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 44
5 to amino acid 53 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

10 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(aa) SEQ ID NO:63, but excluding the poly(A) tail at the
15 3' end of SEQ ID NO:63; and
(ab) the nucleotide sequence of the cDNA insert of clone
pw460_5 deposited under accession number ATCC 98918;

20 (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

25 (b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

30 (ba) SEQ ID NO:63, but excluding the poly(A) tail at the
3' end of SEQ ID NO:63; and
(bb) the nucleotide sequence of the cDNA insert of clone
pw460_5 deposited under accession number ATCC 98918;
(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
(iii) amplifying human DNA sequences; and
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 1147 to nucleotide 1440. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from

15 nucleotide 1234 to nucleotide 1440, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 1234 to nucleotide 1440.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

20 (a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone pw460_5 deposited under accession number ATCC 98918;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

30 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 30 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356; the nucleotide sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356; the nucleotide sequence of the full-length protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918; or the

nucleotide sequence of a mature protein coding sequence of clone qa136_1 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918. In further preferred 5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having 10 biological activity, the fragment comprising the amino acid sequence from amino acid 213 to amino acid 222 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced 15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 20 (aa) SEQ ID NO:65; and
 - (ab) the nucleotide sequence of the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 30 (ba) SEQ ID NO:65; and
 - (bb) the nucleotide sequence of the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a

10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 46 to nucleotide 1356. Also preferably the polynucleotide

15 isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 127 to nucleotide 1356, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide

20 127 to nucleotide 1356.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qa136_1 deposited under accession number ATCC 98918;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 213 to amino acid 222 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624; the nucleotide sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624; the nucleotide sequence of the full-length protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918; or

5 the nucleotide sequence of a mature protein coding sequence of clone qy1261_2 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

10 comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 231

15 to amino acid 240 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

20 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:67, but excluding the poly(A) tail at the

25 3' end of SEQ ID NO:67; and

(ab) the nucleotide sequence of the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

30 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

15 ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624, and extending contiguously from a nucleotide sequence corresponding to the 5' end

20 of said sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 206 to nucleotide 1624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624, and extending contiguously from a

25 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 542 to nucleotide 1624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

30 consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone qy1261_2 deposited under accession number ATCC 98918; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence 10 from amino acid 231 to amino acid 240 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817; the nucleotide sequence of the full-length 10 protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918; or the nucleotide sequence of a mature protein coding sequence of clone rd432_4 deposited under accession number ATCC 98918. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918. In further preferred 15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having 20 biological activity, the fragment comprising the amino acid sequence from amino acid 71 to amino acid 80 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced 25 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 30 (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
 - (ab) the nucleotide sequence of the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

10

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(bb) the nucleotide sequence of the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and

20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide

25 1817, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 1359 to nucleotide 1817.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone rd432_4 deposited under accession number ATCC 98918; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence 10 from amino acid 71 to amino acid 80 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195;
- 20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rb789_14 deposited under accession number ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rb789_14 deposited under accession number ATCC 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:71.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195; the nucleotide sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195; the nucleotide sequence of the full-length protein coding sequence of clone rb789_14 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone rb789_14 deposited

15 under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rb789_14 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological

20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:72.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone
rb789_14 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the
probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the
3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone
rb789_14 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the
25 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide
1195, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:71 from nucleotide 884 to nucleotide 1195, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide
30 884 to nucleotide 1195. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:71 from nucleotide 947 to nucleotide 1195, and extending contiguously from a
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from

nucleotide 947 to nucleotide 1195, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 947 to nucleotide 1195.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

10 rb789_14 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably 15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an 20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd137_1 deposited under accession 25 number ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374; the nucleotide sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374; the nucleotide sequence of the full-length protein

20 coding sequence of clone yd137_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yd137_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004. In further preferred

25 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having

30 biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 15 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and
 - (bb) the nucleotide sequence of the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and 30 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide

374, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 69 to nucleotide 374. Also preferably the polynucleotide isolated according to the above 5 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 186 to nucleotide 374.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the 15 fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yd137_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred 20 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence 25 from amino acid 46 to amino acid 55 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 30 NO:75 from nucleotide 8 to nucleotide 343;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343; the nucleotide sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343; the nucleotide sequence of the full-length protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yd218_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 51
5 to amino acid 60 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

10 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 8 to nucleotide 343. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from

15 nucleotide 50 to nucleotide 343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 50 to nucleotide 343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

20 (a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone yd218_1 deposited under accession number ATCC 207004;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

30 of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679;

5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679; the nucleotide sequence of the full-length protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone ye11_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

of clone ye11_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most 5 preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 261 to amino acid 270 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 10 ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
 - (ab) the nucleotide sequence of the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

25 and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
 - (bb) the nucleotide sequence of the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 84 to nucleotide 1679, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 15 84 to nucleotide 1679.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye11_1 deposited under accession number ATCC 207004;

20 the protein being substantially free from other mammalian proteins. Preferably such 25 protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ 30 ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 261 to amino acid 270 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 30 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646; the nucleotide sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646; the nucleotide sequence of the full-length protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004; or the

nucleotide sequence of a mature protein coding sequence of clone ye72_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004. In further preferred embodiments, the 5 present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the 10 fragment comprising the amino acid sequence from amino acid 257 to amino acid 266 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced 15 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone ye72_1 deposited under accession number ATCC 207004;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone
ye72_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
10 ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 72 to nucleotide 1646. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646, and extending contiguously from a
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 180 to nucleotide 1646.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
25 consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the
fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone
30 ye72_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 257 to amino acid 266 of SEQ ID NO:80.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 10 NO:81 from nucleotide 954 to nucleotide 2423;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye78_1 deposited under accession number 15 ATCC 207004;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye78_1 deposited under accession number ATCC 20 207004;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any 30 one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423; the nucleotide sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423; the nucleotide sequence of the full-length protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone ye78_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;

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(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 954 to nucleotide 2423. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 1224 to nucleotide 2423.

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In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:82;

(b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and

(c) the amino acid sequence encoded by the cDNA insert of clone ye78_1 deposited under accession number ATCC 207004;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

10 of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321;

20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004;

25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321; the nucleotide sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321; the nucleotide sequence of the full-length protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone ye90_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 186 to amino acid 195 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

(ab) the nucleotide sequence of the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

(bb) the nucleotide sequence of the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the

30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 176 to nucleotide 1321, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide

176 to nucleotide 1321. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from 5 nucleotide 233 to nucleotide 1321, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 233 to nucleotide 1321.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:84;
- (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ye90_1 deposited under accession number ATCC 207004;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 186 to amino acid 195 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:85.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605; the nucleotide sequence of the full-length protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yi62_1 deposited under accession number ATCC 207004. In other preferred embodiments, the 25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

5 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605, to a nucleotide 5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 105 to nucleotide 605.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

10 (a) the amino acid sequence of SEQ ID NO:86;
(b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
(c) the amino acid sequence encoded by the cDNA insert of clone yi62_1 deposited under accession number ATCC 207004;

15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

20 of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798;
(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798;

30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798; the nucleotide sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798; the nucleotide sequence of the full-length protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yk78_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004. In further preferred embodiments, the 25 present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the 30

fragment comprising the amino acid sequence from amino acid 91 to amino acid 100 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(ab) the nucleotide sequence of the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 5 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 223 to nucleotide 798. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID 10 NO:87 from nucleotide 430 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 430 to nucleotide 798.

In other embodiments, the present invention provides a composition comprising 15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;
(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
20 (c) the amino acid sequence encoded by the cDNA insert of clone yk78_1 deposited under accession number ATCC 207004; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the 25 amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 91 to amino acid 100 of SEQ ID NO:88.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any 25 one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942; the nucleotide sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942; the nucleotide sequence of the full-length protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yk251_1 deposited under accession number ATCC 207004. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological

5 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:90.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

20 (ab) the nucleotide sequence of the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bb) the nucleotide sequence of the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the

10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 211 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide

15 211 to nucleotide 942. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of

20 said sequence of SEQ ID NO:89 from nucleotide 298 to nucleotide 942.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone yk251_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such

30 protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784; the nucleotide sequence of the full-length

protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004; or the nucleotide sequence of a mature protein coding sequence of clone yt14_1 deposited under accession number ATCC 207004. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert 5 of clone yt14_1 deposited under accession number ATCC 207004. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding 10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 101 to amino acid 110 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 20 consisting of:
 - (aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and
 - (ab) the nucleotide sequence of the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- 30 (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 15 corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 149 to nucleotide 784.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:92;

(b) a fragment of the amino acid sequence of SEQ ID NO:92, the 25 fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone yt14_1 deposited under accession number ATCC 207004;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred 30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 101 to amino acid 110 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441;
- 10 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
- 15 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
- 20 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- 25 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441; the nucleotide sequence of the full-length

protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone bf157_16 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert 5 of clone bf157_16 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding 10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 220 to amino acid 229 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 20 consisting of:
 - (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and
 - (ab) the nucleotide sequence of the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- 30 (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(bb) the nucleotide sequence of the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 15 corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 89 to nucleotide 1441.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:94;

(b) a fragment of the amino acid sequence of SEQ ID NO:94, the 25 fragment comprising eight contiguous amino acids of SEQ ID NO:94; and

(c) the amino acid sequence encoded by the cDNA insert of clone bf157_16 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred 30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 220 to amino acid 229 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629;

10 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

15 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

20 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

25 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629; the nucleotide sequence of the full-length

protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone bk343_2 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert 5 of clone bk343_2 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding 10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 20 consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(bb) the nucleotide sequence of the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 15 corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 219 to nucleotide 629.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

25 (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone bk343_2 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred 30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 63 to amino acid 72 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295;
- 15 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- 20 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- 25 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID

5 NO:97 from nucleotide 556 to nucleotide 951; the nucleotide sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951; the nucleotide sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295; the nucleotide sequence of the full-length protein coding sequence of clone cd205_2 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone cd205_2 deposited 10 under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological 15 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:98.

20 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

25 (i) preparing one or more polynucleotide probes that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
consisting of:

(aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

30 (ab) the nucleotide sequence of the cDNA insert of clone
cd205_2 deposited under accession number ATCC 207088;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

(bb) the nucleotide sequence of the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 556 to nucleotide 951. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 868 to nucleotide 951. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295, and extending contiguously from a nucleotide sequence corresponding

to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 9 to nucleotide 1295.

In other embodiments, the present invention provides a composition comprising 5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone cd205_2 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the 15 amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:98.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 25 NO:99 from nucleotide 216 to nucleotide 443;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1292_8 deposited under accession 30 number ATCC 207088;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.

15 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443; the nucleotide sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443; the nucleotide sequence of the full-length protein coding sequence of clone cw1292_8 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone cw1292_8 deposited 20 under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological 25 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino 30 acid 33 to amino acid 42 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

5 (a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

20 (ab) the nucleotide sequence of the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

30 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

30 (bb) the nucleotide sequence of the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;

35 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

40 (iii) amplifying human DNA sequences; and

45 (iv) isolating the polynucleotide products of step (b)(iii).

50 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 216 to nucleotide 443. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 306 to nucleotide 443.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cw1292_8 deposited under accession number ATCC 207088;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447; the nucleotide sequence of the full-length protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone cw1475_2 deposited under accession number ATCC 207088. In other preferred 30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:102.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

10 (a) a process comprising the steps of:
 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

 (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

15 (ab) the nucleotide sequence of the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;

 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

 (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

 (bb) the nucleotide sequence of the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

 (iii) amplifying human DNA sequences; and

 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447,

10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 2136 to nucleotide 2447.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:102;

(b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw1475_2 deposited under accession number ATCC 207088;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:103.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954; the nucleotide sequence of the full-length protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone dd428_4 deposited under accession number ATCC 207088. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 102 to amino acid 111 of SEQ ID NO:104.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
 - 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
 - (bb) the nucleotide sequence of the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 310 to nucleotide 954.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:104;

(b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and

(c) the amino acid sequence encoded by the cDNA insert of clone dd428_4 deposited under accession number ATCC 207088;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 102 to amino acid 111 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:105.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895; the nucleotide sequence of the full-length protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone dh1073_12 deposited under accession number ATCC 207088. In other preferred 30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:106.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 15 and
- (b) a process comprising the steps of:
 - 20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and
 - (bb) the nucleotide sequence of the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895,

10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 1698 to nucleotide 1895.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone dh1073_12 deposited under accession number ATCC 207088;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:107.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791; the nucleotide sequence of the full-length protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone dw78_1 deposited under accession number ATCC 207088. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:108.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and
 - (bb) the nucleotide sequence of the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but 5 excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791, to a nucleotide 10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 423 to nucleotide 791.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:108;
- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dw78_1 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 56 to amino acid 65 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:109.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944; the nucleotide sequence of the full-length protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone fh116_11 deposited under accession number ATCC 207088. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 136 to amino acid 145 of SEQ ID NO:110.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

10 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

15 (ab) the nucleotide sequence of the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

25 (bb) the nucleotide sequence of the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but 5 excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944, to a nucleotide 10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 96 to nucleotide 944.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fh116_11 deposited under accession number ATCC 207088;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 136 to amino acid 145 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:111.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610; the nucleotide sequence of the full-length protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone fy356_14 deposited under accession number ATCC 207088. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:112.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

10 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

15 (ab) the nucleotide sequence of the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
(iii) isolating the DNA polynucleotides detected with the 20 probe(s);

and

(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 25 3' end of SEQ ID NO:111; and
(bb) the nucleotide sequence of the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;
(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
(iii) amplifying human DNA sequences; and
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 150 to nucleotide 1610.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:112;

(b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and

(c) the amino acid sequence encoded by the cDNA insert of clone fy356_14 deposited under accession number ATCC 207088;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone iw66_1 deposited under accession number ATCC 10 207088;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669; the nucleotide sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669; the nucleotide sequence of the full-length protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088; or the nucleotide sequence of a mature protein coding sequence of clone iw66_1 deposited under accession number ATCC 207088. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088. In further preferred embodiments, the

present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a 5 fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 15 consisting of:
 - (aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and
 - (ab) the nucleotide sequence of the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:113, but excluding the poly(A) tail at the 30 3' end of SEQ ID NO:113; and
 - (bb) the nucleotide sequence of the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and

5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide

10 669, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 49 to nucleotide 669. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

15 NO:113 from nucleotide 112 to nucleotide 669, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 112 to nucleotide 669.

In other embodiments, the present invention provides a composition comprising

20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone iw66_1 deposited under accession number ATCC 207088;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

30 amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416; the nucleotide sequence of the full-length protein coding sequence of clone kh13_4 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone kh13_4

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

5 comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino

10 acid 37 to amino acid 46 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:115, but excluding the poly(A) tail at the

20 3' end of SEQ ID NO:115; and

(ab) the nucleotide sequence of the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:115, but excluding the poly(A) tail at the

30 3' end of SEQ ID NO:115; and

(bb) the nucleotide sequence of the cDNA insert of clone kh13_4 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 165 to nucleotide 416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

(b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and

(c) the amino acid sequence encoded by the cDNA insert of clone 25 kh13_4 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 30 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602; the nucleotide sequence of the full-length protein coding sequence of clone ko258_4 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone ko258_4

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein 5 comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino 10 acid 61 to amino acid 70 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(aa) SEQ ID NO:117, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:117; and
(ab) the nucleotide sequence of the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
25 (iii) isolating the DNA polynucleotides detected with the probe(s);
and
(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(ba) SEQ ID NO:117, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:117; and

(bb) the nucleotide sequence of the cDNA insert of clone ko258_4 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 204 to nucleotide 602.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone 25 ko258_4 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:118.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:119.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739; the nucleotide sequence of the full-length protein coding sequence of clone kv10_8 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone kv10_8

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:119.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:119, but excluding the poly(A) tail at the 20 3' end of SEQ ID NO:119; and
 - (ab) the nucleotide sequence of the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the 25 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that 30 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

(bb) the nucleotide sequence of the cDNA insert of clone kv10_8 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:119 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 434 to nucleotide 739.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:120;

(b) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and

(c) the amino acid sequence encoded by the cDNA insert of clone 25 kv10_8 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:120.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:122;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:122;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:121.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310; the nucleotide sequence of the full-length protein coding sequence of clone LL89_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone LL89_3

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

5 comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty contiguous amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino

10 acid 22 to amino acid 31 of SEQ ID NO:122.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(ab) the nucleotide sequence of the cDNA insert of clone LL89_3 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(bb) the nucleotide sequence of the cDNA insert of clone
LL89_3 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 149 to nucleotide 310.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:122;

(b) a fragment of the amino acid sequence of SEQ ID NO:122, the
fragment comprising eight contiguous amino acids of SEQ ID NO:122; and

(c) the amino acid sequence encoded by the cDNA insert of clone

25 LL89_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:122.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:124;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:123.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288; the nucleotide sequence of the full-length protein coding sequence of clone mc300_1 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone mc300_1

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein 5 comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino 10 acid 39 to amino acid 48 of SEQ ID NO:124.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(aa) SEQ ID NO:123, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:123; and
(ab) the nucleotide sequence of the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
25 (iii) isolating the DNA polynucleotides detected with the probe(s);
and
(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
30 (ba) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

(bb) the nucleotide sequence of the cDNA insert of clone mc300_1 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:123 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 22 to nucleotide 288.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:124;

(b) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and

(c) the amino acid sequence encoded by the cDNA insert of clone 25 mc300_1 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:124.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:125.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449; the nucleotide sequence of the full-length protein coding sequence of clone ml227_1 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone ml227_1

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

5 comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino

10 acid 370 to amino acid 379 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:125.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(ab) the nucleotide sequence of the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(bb) the nucleotide sequence of the cDNA insert of clone ml227_1 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:125 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 200 to nucleotide 2449.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:126;

(b) a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and

(c) the amino acid sequence encoded by the cDNA insert of clone

25 ml227_1 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a protein comprising a fragment of the amino acid sequence of SEQ 30 ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 370 to amino acid 379 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:127.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980; the nucleotide sequence of the full-length protein coding sequence of clone mm367_6 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone mm367_6

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 311 to amino acid 320 of SEQ ID NO:128.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:127.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(aa) SEQ ID NO:127, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:127; and
(ab) the nucleotide sequence of the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(ba) SEQ ID NO:127, but excluding the poly(A) tail at the
3' end of SEQ ID NO:127; and

(bb) the nucleotide sequence of the cDNA insert of clone mm367_6 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:127 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 82 to nucleotide 1980.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:128;

(b) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and

(c) the amino acid sequence encoded by the cDNA insert of clone 25 mm367_6 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 311 to amino acid 320 of SEQ ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 30 25% of the length of SEQ ID NO:129.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856; the nucleotide sequence of the full-length protein coding sequence of clone mt124_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone mt124_3

deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein 5 comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino 10 acid 117 to amino acid 126 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

15 (a) a process comprising the steps of:
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
(aa) SEQ ID NO:129, but excluding the poly(A) tail at the
20 3' end of SEQ ID NO:129; and
(ab) the nucleotide sequence of the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
25 (iii) isolating the DNA polynucleotides detected with the probe(s);
and
(b) a process comprising the steps of:
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
30 (ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and

(bb) the nucleotide sequence of the cDNA insert of clone mt124_3 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 10 ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856, and extending contiguously from a nucleotide sequence corresponding to the 5' end 15 of said sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 125 to nucleotide 856.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 20 consisting of:

(a) the amino acid sequence of SEQ ID NO:130;

(b) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(c) the amino acid sequence encoded by the cDNA insert of clone 25 mt124_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:130.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:131.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940; the nucleotide sequence of SEQ ID

NO:131 from nucleotide 901 to nucleotide 2940; the nucleotide sequence of the full-length protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone nf56_3 deposited under accession number ATCC 207089. In other preferred embodiments, the 5 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most 10 preferably thirty) contiguous amino acids of SEQ ID NO:132, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 342 to amino acid 351 of SEQ ID NO:132.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 15 ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize 20 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and
 - (ab) the nucleotide sequence of the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 30 and
 - (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

(bb) the nucleotide sequence of the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 15 corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 856 to nucleotide 2940. Also preferably the polynucleotide isolated according to the above 20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 901 to nucleotide 2940.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:132;

(b) a fragment of the amino acid sequence of SEQ ID NO:132, the 30 fragment comprising eight contiguous amino acids of SEQ ID NO:132; and

(c) the amino acid sequence encoded by the cDNA insert of clone nf56_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:132. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a protein comprising a fragment of the amino acid sequence of SEQ 5 ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 342 to amino acid 351 of SEQ ID NO:132.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 10 NO:133;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:133.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448; the nucleotide sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448; the nucleotide sequence of the full-length protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089; or

10 the nucleotide sequence of a mature protein coding sequence of clone qy442_2 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

15 comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino

20 acid 49 to amino acid 58 of SEQ ID NO:134.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

25 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:133, but excluding the poly(A) tail at the

30 3' end of SEQ ID NO:133; and

(ab) the nucleotide sequence of the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:133, but excluding the poly(A) tail at the 3' end of SEQ ID NO:133; and

10 (bb) the nucleotide sequence of the cDNA insert of clone qy442_2 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:133, but 20 excluding the poly(A) tail at the 3' end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448, to a nucleotide 25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 122 to nucleotide 448. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 167 to nucleotide 448. 30

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:134;
- (b) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and
- (c) the amino acid sequence encoded by the cDNA insert of clone 5 qy442_2 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an 15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rj214_14 deposited under accession 20 number ATCC 207089;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:136;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:136;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:135.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777; the nucleotide sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777; the nucleotide sequence of the full-length protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone rj214_14 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:136, or a polynucleotide 20 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:136.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:135.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:135, but excluding the poly(A) tail at the

3' end of SEQ ID NO:135; and

(ab) the nucleotide sequence of the cDNA insert of clone
rj214_14 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the
probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from
the group consisting of:

(ba) SEQ ID NO:135, but excluding the poly(A) tail at the

3' end of SEQ ID NO:135; and

20 (bb) the nucleotide sequence of the cDNA insert of clone
rj214_14 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ
ID NO:135 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the

30 polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide
777, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:135 from nucleotide 28 to nucleotide 777, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:135 from nucleotide

28 to nucleotide 777. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:135 from 5 nucleotide 73 to nucleotide 777, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:135 from nucleotide 73 to nucleotide 777.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:136;
- (b) a fragment of the amino acid sequence of SEQ ID NO:136, the fragment comprising eight contiguous amino acids of SEQ ID NO:136; and
- (c) the amino acid sequence encoded by the cDNA insert of clone rj214_14 deposited under accession number ATCC 207089;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:136. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:136, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:136 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:136.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:138;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:138;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any 20 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:137.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745; the nucleotide sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745; the nucleotide sequence of the full-length protein 25 coding sequence of clone rk80_3 deposited under accession number ATCC 207089; or the nucleotide sequence of a mature protein coding sequence of clone rk80_3 deposited under accession number ATCC 207089. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089. In further preferred embodiments, the 30 present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:138, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the

fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:138.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:137.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

15

(ab) the nucleotide sequence of the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137; and

(bb) the nucleotide sequence of the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:137 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:137, but excluding the poly(A) tail at the 3' end of SEQ ID NO:137. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 5 745, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 179 to nucleotide 745. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID 10 NO:137 from nucleotide 233 to nucleotide 745, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:137 from nucleotide 233 to nucleotide 745.

In other embodiments, the present invention provides a composition comprising 15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:138;
- (b) a fragment of the amino acid sequence of SEQ ID NO:138, the fragment comprising eight contiguous amino acids of SEQ ID NO:138; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone rk80_3 deposited under accession number ATCC 207089;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the 25 amino acid sequence of SEQ ID NO:138 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:138, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:138 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:138.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone au36_42 deposited under accession number ATCC 207187;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone au36_42 deposited under accession number 10 ATCC 207187;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:140;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:140;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any 25 one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:139.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274; the nucleotide sequence of the full-length protein coding sequence of clone au36_42 deposited under accession number 30 ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone au36_42 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone au36_42 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding

a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:140, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140

5 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:140.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:139.

Further embodiments of the invention provide isolated polynucleotides produced

10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and

(ab) the nucleotide sequence of the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139; and

30 (bb) the nucleotide sequence of the cDNA insert of clone au36_42 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ 5 ID NO:139 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:139, but excluding the poly(A) tail at the 3' end of SEQ ID NO:139. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274, 10 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:139 from nucleotide 1017 to nucleotide 1274.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group 15 consisting of:

- (a) the amino acid sequence of SEQ ID NO:140;
- (b) a fragment of the amino acid sequence of SEQ ID NO:140, the fragment comprising eight contiguous amino acids of SEQ ID NO:140; and
- (c) the amino acid sequence encoded by the cDNA insert of clone 20 au36_42 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:140. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment preferably 25 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:140, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:140 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:140.

In one embodiment, the present invention provides a composition comprising an 30 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:142;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:142;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:141.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774; the nucleotide sequence of the full-length protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone bo549_13 deposited under accession number ATCC 207187. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:142, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 27 to amino acid 36 of SEQ ID NO:142.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:141.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141; and

15 (ab) the nucleotide sequence of the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:141, but excluding the poly(A) tail at the 3' end of SEQ ID NO:141; and

(bb) the nucleotide sequence of the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:141 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:141, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:141. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774; to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:141 from nucleotide 580 to nucleotide 774.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:142;

(b) a fragment of the amino acid sequence of SEQ ID NO:142, the fragment comprising eight contiguous amino acids of SEQ ID NO:142; and

(c) the amino acid sequence encoded by the cDNA insert of clone bo549_13 deposited under accession number ATCC 207187;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:142. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:142, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:142 having biological activity, the fragment comprising the amino acid sequence from amino acid 27 to amino acid 36 of SEQ ID NO:142.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone da529_3 deposited under accession number ATCC 207187;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone da529_3 deposited under accession number ATCC 207187;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:144;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:144;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any 25 one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:143.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969; the nucleotide sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969; the nucleotide sequence of the full-length protein coding sequence of clone da529_3 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone da529_3 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:144, or a polynucleotide 5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 128 to amino acid 137 of SEQ ID NO:144.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:143.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 15 consisting of:

(aa) SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143; and

(ab) the nucleotide sequence of the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:143, but excluding the poly(A) tail at the 30 3' end of SEQ ID NO:143; and

(bb) the nucleotide sequence of the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143, and

5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:143 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:143, but excluding the poly(A) tail at the 3' end of SEQ ID NO:143. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide

10 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 172 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

15 NO:143 from nucleotide 385 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:143 from nucleotide 385 to nucleotide 969.

In other embodiments, the present invention provides a composition comprising

20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:144;
- (b) a fragment of the amino acid sequence of SEQ ID NO:144, the fragment comprising eight contiguous amino acids of SEQ ID NO:144; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone da529_3 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:144. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

30 amino acid sequence of SEQ ID NO:144 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:144, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:144 having biological activity, the fragment comprising the amino acid sequence from amino acid 128 to amino acid 137 of SEQ ID NO:144.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:146;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:146;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of 25 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:145.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667; the nucleotide sequence of SEQ ID NO:145

from nucleotide 368 to nucleotide 667; the nucleotide sequence of the full-length protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone dm365_3 deposited under accession number ATCC 207187. In other preferred embodiments, the 5 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most 10 preferably thirty) contiguous amino acids of SEQ ID NO:146, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:146.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:145.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and
 - (ab) the nucleotide sequence of the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);

30 and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145; and

(bb) the nucleotide sequence of the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a 10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:145 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:145, but excluding the poly(A) tail at the 3' end of SEQ ID NO:145. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence 15 corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 329 to nucleotide 667. Also preferably the polynucleotide isolated according to the above 20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:145 from nucleotide 368 to nucleotide 667.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:146;

(b) a fragment of the amino acid sequence of SEQ ID NO:146, the 30 fragment comprising eight contiguous amino acids of SEQ ID NO:146; and

(c) the amino acid sequence encoded by the cDNA insert of clone dm365_3 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:146. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:146 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:146, or a protein comprising a fragment of the amino acid sequence of SEQ 5 ID NO:146 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:146.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID 10 NO:147;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fa171_1 deposited under accession 15 number ATCC 207187;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fa171_1 deposited under accession number 20 ATCC 207187;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:148;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:148;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of 25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:147.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368; the nucleotide sequence of the full-length protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone fa171_1 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:148, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 206 to amino acid 215 of SEQ ID NO:148.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:147.

20 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

25 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

(ab) the nucleotide sequence of the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;

30 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147; and

(bb) the nucleotide sequence of the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in 10 conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147, and 15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:147 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:147, but excluding the poly(A) tail at the 3' end of SEQ ID NO:147. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 20 1368, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:147 from nucleotide 103 to nucleotide 1368.

In other embodiments, the present invention provides a composition comprising 25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:148;

(b) a fragment of the amino acid sequence of SEQ ID NO:148, the fragment comprising eight contiguous amino acids of SEQ ID NO:148; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone fa171_1 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:148. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:148 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:148, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:148 having biological activity, the fragment comprising the amino acid sequence from amino acid 206 to amino acid 215 of SEQ ID NO:148.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:150;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:150;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:149.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407; the nucleotide sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407; the nucleotide sequence of the full-length protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone lp572_2 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:150, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:150.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:149.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

(ab) the nucleotide sequence of the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5

(ba) SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149; and

(bb) the nucleotide sequence of the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;

10

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:149 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:149, but excluding the poly(A) tail at the 3' end of SEQ ID NO:149. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 190 to nucleotide 1407. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:149 from nucleotide 463 to nucleotide 1407.

20

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:150;

(b) a fragment of the amino acid sequence of SEQ ID NO:150, the fragment comprising eight contiguous amino acids of SEQ ID NO:150; and

(c) the amino acid sequence encoded by the cDNA insert of clone lp572_2 deposited under accession number ATCC 207187;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:150. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

10 of SEQ ID NO:150, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:150 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:150.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035;

20 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:152;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:152;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:151.

15 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035; the nucleotide sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035; the nucleotide sequence of the full-length protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone pe246_1 deposited under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:152, or a polynucleotide 20 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:152.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:151.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(ab) the nucleotide sequence of the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151; and

(bb) the nucleotide sequence of the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:151 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:151, but excluding the poly(A) tail at the 3' end of SEQ ID NO:151. Also preferably the 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from nucleotide 301 to nucleotide 1035, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide

301 to nucleotide 1035. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:151 from 5 nucleotide 916 to nucleotide 1035, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:151 from nucleotide 916 to nucleotide 1035.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:152;
- (b) a fragment of the amino acid sequence of SEQ ID NO:152, the fragment comprising eight contiguous amino acids of SEQ ID NO:152; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pe246_1 deposited under accession number ATCC 207187;

15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:152. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

20 of SEQ ID NO:152, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:152 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:152.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:154;
- 10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:154;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:153.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281; the nucleotide sequence of the full-length protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone qf122_3 deposited under accession number ATCC 207187. In other preferred embodiments, the

25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:154, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:154.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:153.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

5 (a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

 - (aa) SEQ ID NO:153; and
 - (ab) the nucleotide sequence of the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

10 and

(b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

 - (ba) SEQ ID NO:153; and
 - (bb) the nucleotide sequence of the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:153 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:153. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281, and extending contiguously from a nucleotide sequence

corresponding to the 5' end of said sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:153 from nucleotide 94 to nucleotide 1281.

In other embodiments, the present invention provides a composition comprising 5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:154;
- (b) a fragment of the amino acid sequence of SEQ ID NO:154, the fragment comprising eight contiguous amino acids of SEQ ID NO:154; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone qf122_3 deposited under accession number ATCC 207187;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:154. In further preferred embodiments, the present invention provides a protein comprising a fragment of the 15 amino acid sequence of SEQ ID NO:154 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:154, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:154 having biological activity, the fragment comprising the amino acid sequence from amino acid 193 to amino acid 202 of SEQ ID NO:154.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 25 NO:155 from nucleotide 110 to nucleotide 742;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qv538_1 deposited under accession 30 number ATCC 207187;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:155.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742; the nucleotide sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742; the nucleotide sequence of the full-length protein coding sequence of clone qv538_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone qv538_1 deposited 25 under accession number ATCC 207187. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological 30 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:156.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:155.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

5 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:155, but excluding the poly(A) tail at the 10 3' end of SEQ ID NO:155; and

(ab) the nucleotide sequence of the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155; and

(bb) the nucleotide sequence of the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155, but excluding the poly(A) tail at the 3' end of SEQ ID NO:155. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 110 to nucleotide 742. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 170 to nucleotide 742.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:156;
- (b) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qv538_1 deposited under accession number ATCC 207187;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:156.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:158;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:158;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:157.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757; the nucleotide sequence of the full-length protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187; or the nucleotide sequence of a mature protein coding sequence of clone ys20_1 deposited under accession number ATCC 207187. In other preferred embodiments, the

30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:158, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:158.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:157.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

15 (ab) the nucleotide sequence of the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(bb) the nucleotide sequence of the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:157 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but

5 excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757, to a nucleotide

10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:157 from nucleotide 41 to nucleotide 757.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

15 (a) the amino acid sequence of SEQ ID NO:158;

(b) a fragment of the amino acid sequence of SEQ ID NO:158, the fragment comprising eight contiguous amino acids of SEQ ID NO:158; and

(c) the amino acid sequence encoded by the cDNA insert of clone ys20_1 deposited under accession number ATCC 207187;

20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:158. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

25 of SEQ ID NO:158, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:158 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:158.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:160;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:160;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:159.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253; the nucleotide sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253; the nucleotide sequence of the full-length protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX; or the nucleotide sequence of a mature protein coding sequence of clone as180_1 deposited under accession number ATCC XXXXXX. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX. In further

preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:160, or a polynucleotide 5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 366 to amino acid 375 of SEQ ID NO:160.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:159.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group 15 consisting of:
 - (aa) SEQ ID NO:159; and
 - (ab) the nucleotide sequence of the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:159; and
 - (bb) the nucleotide sequence of the cDNA insert of clone 25 as180_1 deposited under accession number ATCC XXXXXX;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
 - (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:159 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:159. Also

5 preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:159 from nucleotide 28 to nucleotide 2253, to a nucleotide sequence corresponding to the 3' end of said sequence of

10 SEQ ID NO:159 from nucleotide 28 to nucleotide 2253. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253, to a nucleotide

15 sequence corresponding to the 3' end of said sequence of SEQ ID NO:159 from nucleotide 568 to nucleotide 2253.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

20 (a) the amino acid sequence of SEQ ID NO:160;

(b) a fragment of the amino acid sequence of SEQ ID NO:160, the fragment comprising eight contiguous amino acids of SEQ ID NO:160; and

(c) the amino acid sequence encoded by the cDNA insert of clone as180_1 deposited under accession number ATCC XXXXXX;

25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

30 of SEQ ID NO:160, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:160 having biological activity, the fragment comprising the amino acid sequence from amino acid 366 to amino acid 375 of SEQ ID NO:160.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial,

yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

5 Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present
10 invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical
15 condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

20 Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

Figure 2 is a schematic representation of the pCMV Sport2 vector used for deposit of clone qs14_3 disclosed herein.

25 DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone
30 in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have

determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

10 Clone "co62_12"

A polynucleotide of the present invention has been identified as clone "co62_12". co62_12 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 15 analysis of the amino acid sequence of the encoded protein. co62_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co62_12 protein").

The nucleotide sequence of co62_12 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper 20 reading frame and the predicted amino acid sequence of the co62_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 1 to 11 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 12. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain 25 should the predicted leader/signal sequence not be separated from the remainder of the co62_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co62_12 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for co62_12 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co62_12 demonstrated at least some similarity with sequences identified as AA019597 (ze60f10.s1 Soares retina N2b4HR Homo sapiens cDNA), AA021678 (mh82c02.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus), AA057573 (zf62d10.s1 Soares retina N2b4HR Homo sapiens cDNA clone 381523 3' similar to WP

T12G3.4 CE06440 STRICTOSIDINE SYNTHASE LIKE, mRNA sequence), AA130982, AA287697 (zs53g02.r1 Soares NbHTGBC Homo sapiens cDNA clone 701234 5'), AI042188 (oy37d10.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668019 3' similar to WP:F57C2.5 CE16156, mRNA sequence), R63905 (yi19b03.s1

5 Homo sapiens cDNA clone 139661 3'), T03538 (IB43 Infant brain, Bento Soares Homo sapiens cDNA clone IB43 3'end), T20257 (Human gene signature HUMGS01405), and T23663 (seq294 Homo sapiens cDNA clone b4HB3MA-Cot109+103-Bio-24 3'). The predicted amino acid sequence disclosed herein for co62_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

10 The predicted co62_12 protein demonstrated at least some similarity to sequences identified as R88502 (Protein sequence for mediating male fertility in plants) and Z83110 (F57C2.5 [Caenorhabditis elegans]). Based upon sequence similarity, co62_12 proteins and each similar protein or peptide may share at least some activity.

15 Clone "lo311_8"

A polynucleotide of the present invention has been identified as clone "lo311_8". lo311_8 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. lo311_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lo311_8 protein").

The nucleotide sequence of lo311_8 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lo311_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 17 to 29 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain. 30 should the predicted leader/signal sequence not be separated from the remainder of the lo311_8 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lo311_8 should be approximately 3850 bp.

The nucleotide sequence disclosed herein for lo311_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. lo311_8 demonstrated at least some similarity with sequences identified as AA046836 (zf14b10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA 5 clone 376891 5' similar to WP:ZK686.3 CE00457), AA297716 (EST113273 Infant adrenal gland, subtracted (total cDNA) I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK686_3), AF008554 (Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds), T68050 (yc39h10.r1 Homo sapiens cDNA clone 83107 5' similar to SP ZK686.3 CE00457), and U42349 (Human N33 mRNA, complete cds). The predicted amino acid sequence disclosed herein for lo311_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted lo311_8 protein demonstrated at least some similarity to sequences identified as AF008554 (implantation-associated protein [Rattus norvegicus]), R85333 (Human prostate/colon tumour suppressor protein form 1) and 15 U42349 (39 kDa encoded by N33 [Homo sapiens]). Based upon sequence similarity, lo311_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the lo311_8 protein sequence, centered around amino acids 10, 190, 220, 275, and 310 of SEQ ID NO:4, respectively.

20

Clone "ns197_1"

A polynucleotide of the present invention has been identified as clone "ns197_1". ns197_1 was isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. 25 No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ns197_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ns197_1 protein").

The nucleotide sequence of ns197_1 as presently determined is reported in SEQ 30 ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ns197_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ns197_1 should be approximately 3650 bp.

The nucleotide sequence disclosed herein for ns197_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ns197_1 demonstrated at least some similarity with sequences identified as AA495135 (fa03c11.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 3K8 5' 5 similar to WP:ZC518.3 CE06603 ALCOHOL DEHYDROGENASE TRANSCRIPTION EFFECTOR LIKE; mRNA sequence). The predicted amino acid sequence disclosed herein for ns197_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ns197_1 protein demonstrated at least some similarity to the sequence identified as Z68753 (ZC518.3 10 [Caenorhabditis elegans]). Based upon sequence similarity, ns197_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ns197_1 protein sequence centered around amino acid 135 of SEQ ID NO:6. The nucleotide sequence of ns197_1 indicates that it may contain one or more repeat sequences, including primate simple 15 repeat GCC, Alu, and other repetitive elements.

Clone "pj193_5"

A polynucleotide of the present invention has been identified as clone "pj193_5". pj193_5 was isolated from a human fetal carcinoma (NTD2 cells, treated with retinoic acid 20 for 23 days) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj193_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj193_5 protein").

25 The nucleotide sequence of pj193_5 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj193_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 9 to 21 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted 30 mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pj193_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pj193_5 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for pj193_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 5 FASTA search protocols. pj193_5 demonstrated at least some similarity with sequences identified as AA296889 (EST112653 Cerebellum II Homo sapiens cDNA 5' end), AA296961 (EST112514 Adrenal gland tumor Homo sapiens cDNA 5' end), AA661635 (nv02g06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219066), and U80744 (Homo sapiens CTG4a mRNA, complete cds). The predicted amino acid sequence disclosed 10 herein for pj193_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pj193_5 protein demonstrated at least some similarity to the sequence identified as U80744 (CTG4a [Homo sapiens]). Based upon sequence similarity, pj193_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of pj193_5 indicates 15 that it may contain CAG nucleotide repeats; these repeats may create a "hotspot" for certain types of mutations. "Twelve diseases, most with neuropsychiatric features, arise from trinucleotide repeat expansion mutations. Expansion mutations may also cause a number of other disorders, including several additional forms of spinocerebellar ataxia, bipolar affective disorder, schizophrenia, and autism." (Margolis *et al.*, 1997, *Human 20 Genetics* 100(1): 114-122, which is incorporated by reference herein.) It is possible that the gene corresponding to pj193_5 undergoes a similar etiology.

pj193_5 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 31 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

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Clone "pj317_2"

A polynucleotide of the present invention has been identified as clone "pj317_2". pj317_2 was isolated from a human fetal carcinoma (NTD2 cells, treated with retinoic acid for 23 days) cDNA library using methods which are selective for cDNAs encoding 30 secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pj317_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pj317_2 protein").

The nucleotide sequence of pj317_2 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pj317_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pj317_2 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pj317_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pj317_2 demonstrated at least some similarity with sequences 10 identified as AA305508 (EST176494 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence), AA471379 (PMY1151 KG1a Lambda Zap Express cDNA Library Homo sapiens cDNA 5', mRNA sequence), and AA906311 (ok03f08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506759 3', mRNA sequence). The predicted amino acid sequence disclosed herein for pj317_2 was searched against the 15 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pj317_2 protein demonstrated at least some similarity to the sequences identified as U37763 (Per9p [Pichia angusta]) and U56965 (Caenorhabditis elegans cosmid C15H9). Per9p is a peroxisomal membrane protein, and the predicted pj317_2 protein demonstrated at least some similarity to peroxisomal proteins from other species as well. 20 Based upon sequence similarity, pj317_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pj317_2 protein sequence centered around amino acid 25 of SEQ ID NO:10. The nucleotide sequence of pj317_2 indicates that it may contain a simple AT and MER repeat region.

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Clone "pt332_1"

A polynucleotide of the present invention has been identified as clone "pt332_1". pt332_1 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. 30 Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pt332_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt332_1 protein").

The nucleotide sequence of pt332_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt332_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino 5 acids 287 to 299 of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 300. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt332_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt332_1 should be approximately 3450 bp.

The nucleotide sequence disclosed herein for pt332_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pt332_1 demonstrated at least some similarity with sequences 15 identified as AA167221 (zp13c09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 609328 3'), AA437109 (zv53c07.s1 Soares testis NHT Homo sapiens cDNA clone 757356 3'), H14107 (ym62a06.r1 Homo sapiens cDNA clone 163474 5'), and U41264 (C. elegans cDNA). Based upon sequence similarity, pt332_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program 20 predicts a potential transmembrane domain within the pt332_1 protein sequence centered around amino acid 270 of SEQ ID NO:12.

pt332_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 100 kDa was detected in membrane fractions using SDS 25 polyacrylamide gel electrophoresis.

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Clone "qc297_15"

A polynucleotide of the present invention has been identified as clone "qc297_15". qc297_15 was isolated from a human adult neural (neuroepithelioma HTB-10 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins 30 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qc297_15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qc297_15 protein").

The nucleotide sequence of qc297_15 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qc297_15 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qc297_15 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for qc297_15 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qc297_15 demonstrated at least some similarity with sequences 10 identified as AA625537 (af72g07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 1047612 5') and T24537 (EST112 Homo sapiens cDNA clone 4H3). Based upon sequence similarity, qc297_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the qc297_15 protein sequence, around amino acid 20 of SEQ ID NO:14. The 15 nucleotide/amino acid sequence of qc297_15 indicates that it may contain an Alu/SVA/MER repeat region.

qc297_15 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 7 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

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Clone "qg596_12"

A polynucleotide of the present invention has been identified as clone "qg596_12". qg596_12 was isolated from a human adult neural (neuroepithelioma HTB-10 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins 25 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qg596_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qg596_12 protein").

The nucleotide sequence of qg596_12 as presently determined is reported in SEQ 30 ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qg596_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qg596_12 should be approximately 2750 bp.

The nucleotide sequence disclosed herein for qg596_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qg596_12 demonstrated at least some similarity with sequences identified as AA332939 (EST37132 Embryo, 8 week I Homo sapiens cDNA 5' end),
5 AA334678 (EST39190 Embryo, 9 week Homo sapiens cDNA 5' end), AA362653 (EST72375 Namalwa B cells I Homo sapiens cDNA 5' end), and AA829841 (od40d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370401 3' similar to WP:F10G7.1 CE02624). The predicted amino acid sequence disclosed herein for qg596_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX 10 search protocol. The predicted qg596_12 protein demonstrated at least some similarity to the sequence identified as U40029 (coded for by C. elegans cDNA yk16b1.3; coded for by C. elegans cDNA yk8g6.5; coded for by C. elegans cDNA yk8g6.3; coded for by C. elegans cDNA yk6d3.5). Based upon sequence similarity, qg596_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer 15 program predicts two potential transmembrane domains within the qg596_12 protein sequence, one centered around amino acid 180 and another around amino acid 660 of SEQ ID NO:16.

qg596_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 33 kDa was detected in membrane fractions using SDS 20 polyacrylamide gel electrophoresis.

Clone "rb649_3"

A polynucleotide of the present invention has been identified as clone "rb649_3". rb649_3 was isolated from a human fetal kidney (293 cell line) cDNA library using 25 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rb649_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rb649_3 protein").

30 The nucleotide sequence of rb649_3 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rb649_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 42 to 54 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted

mature amino acid sequence beginning at amino acid 55. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rb649_3 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rb649_3 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for rb649_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rb649_3 demonstrated at least some similarity with sequences 10 identified as AA177001 (nc01h02.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE 182). The predicted amino acid sequence disclosed herein for rb649_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted rb649_3 protein demonstrated at least some similarity to sequences identified as AB002405 (LAK-4p [Homo sapiens]), R89470 (Collagen/TGF-beta- 15 1 fusion protein), and U23516 (Undefined [Caenorhabditis elegans]). Based upon sequence similarity, rb649_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eight additional potential transmembrane domains within the rb649_3 protein sequence, centered around amino acids 140, 240, 280, 325, 370, 425, 475, and 540 of SEQ ID NO:18, respectively. The 20 nucleotide sequence of rb649_3 indicates that it may contain a simple GGA repeat region.

Clone "ca106_19x"

A polynucleotide of the present invention has been identified as clone "ca106_19x". A cDNA clone was first isolated from a mouse embryonic (ES cell embryoid bodies 25 harvested 2-12 days after LIF removed) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate ca106_19x from a mixture of human fetal brain and human adult brain cDNA libraries. 30 ca106_19x is a full-length human clone, including the entire coding sequence of a secreted protein (also referred to herein as "ca106_19x protein").

The nucleotide sequence of ca106_19x as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the ca106_19x protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ca106_19x should be approximately 4050 bp.

5 The nucleotide sequence disclosed herein for ca106_19x was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ca106_19x demonstrated at least some similarity with sequences identified as AA886998 (oj30g03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1499860 3'), F08279 (H. sapiens partial cDNA sequence; clone c-zpe11), F13022 (H.
10 sapiens partial cDNA sequence; clone c-3hf07), H38128 (yp46c12.s1 Homo sapiens cDNA clone 190486 3'), T77601 (yc91e07.r1 Homo sapiens cDNA clone 23192 5'), U93720 (Homo sapiens TEX28 mRNA, complete cds), W55512 (ma28h03.r1 Life Tech mouse brain Mus musculus cDNA clone 312053 5'), and Z22333 (H.sapiens DNA sequence). The predicted amino acid sequence disclosed herein for ca106_19x was searched against the GenPept
15 and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ca106_19x protein demonstrated at least some similarity to sequences identified as U56965 (C15H9.4 gene product [Caenorhabditis elegans]) and U93720 (TEX28 [Homo sapiens]). Based upon sequence similarity, ca106_19x proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts
20 four potential transmembrane domains within the ca106_19x protein sequence, centered around amino acids 170, 430, 590, and 625 of SEQ ID NO:20, respectively. The nucleotide sequence of ca106_19x indicates that it contains at least one repetitive element.

Clone "ci52_2"

25 A polynucleotide of the present invention has been identified as clone "ci52_2". A cDNA clone was first isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then
30 used to isolate ci52_2 from a human fetal brain cDNA library. ci52_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ci52_2 protein").

The nucleotide sequence of ci52_2 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the ci52_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 9 to 21 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the 5 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ci52_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ci52_2 should be approximately 1775 bp.

10 The nucleotide sequence disclosed herein for ci52_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ci52_2 demonstrated at least some similarity with sequences identified as AA083339 (zn31d10.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 549043 5'), AA514339 (nf56c10.s1 NCI_CGAP_Co3 Homo sapiens cDNA 15 clone 923922), AA628942 (af28f01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 1032985 3', mRNA sequence), M78692 (EST00840 Homo sapiens cDNA clone HHCMC16), N67265 (yz49d04.s1 Homo sapiens cDNA clone 286375 3'), N95514 (yy62d10.r1 Homo sapiens cDNA clone 278131 5'), Q60715 (Human brain Expressed Sequence Tag EST00840; standard; cDNA), and R46588 (yg51a12.s1 Homo sapiens cDNA 20 clone 35984 3'). The predicted amino acid sequence disclosed herein for ci52_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ci52_2 protein demonstrated at least some similarity to the sequence identified as M68866 (stranded at second [Drosophila melanogaster]). Based upon sequence similarity, ci52_2 proteins and each similar protein 25 or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the ci52_2 protein sequence, one around amino acid 146 and another around amino acid 177 of SEQ ID NO:22.

Clone "md124_16"

30 A polynucleotide of the present invention has been identified as clone "md124_16". A cDNA clone was first isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then

used to isolate md124_16 from a human adult kidney cDNA library. md124_16 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "md124_16 protein").

The nucleotide sequence of md124_16 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the md124_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 152 to 164 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 165. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the md124_16 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone md124_16 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for md124_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. md124_16 demonstrated at least some similarity with sequences identified as AA215643 (zr98d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683721 3'), AA489121 (aa56b07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824917 5'), W72865 (zd59e07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344964 3'), and W76100 (zd59e07.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344964 5'). Based upon sequence similarity, md124_16 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of md124_16 indicates that it may contain at least one MER repeat sequence.

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Clone "pk366_7"

A polynucleotide of the present invention has been identified as clone "pk366_7". pk366_7 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pk366_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pk366_7 protein").

The nucleotide sequence of pk366_7 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pk366_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 361 to 373 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 374. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pk366_7 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pk366_7 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for pk366_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pk366_7 demonstrated at least some similarity with sequences identified as AA057428 (zf57c11.s1 Soares retina N2b4HR Homo sapiens cDNA clone 381044 3'), AA457625 (aa89e09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 838504 5'), AA601545 (nn87h11.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1098213), T19564 (Human gene signature HUMGS00629; standard; cDNA to mRNA), and U94831 (Homo sapiens multispanning membrane protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for pk366_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pk366_7 protein demonstrated at least some similarity to sequences identified as D87444 (endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]), U94831 (multispanning membrane protein [Homo sapiens]), and U95973 (endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]). Based upon sequence similarity, pk366_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts nine additional potential transmembrane domains within the pk366_7 protein sequence, centered around amino acids 191, 260, 288, 325, 355, 412, 447, 481, and 517 of SEQ ID NO:26, respectively.

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Clone "pl741_5"

A polynucleotide of the present invention has been identified as clone "pl741_5". pl741_5 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.

5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pl741_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pl741_5 protein").

5 The nucleotide sequence of pl741_5 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pl741_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 3 to 15 of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted 10 mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pl741_5 protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pl741_5 should be approximately 3000 bp.

16 The nucleotide sequence disclosed herein for pl741_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pl741_5 demonstrated at least some similarity with sequences identified as AA283176 (zt17a04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713358 3'), AA204801 (zq61d12.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 646103 5'), and H59410 (yr19g04.r1 Homo sapiens cDNA clone 205782 5'). The predicted amino acid sequence disclosed herein for pl741_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pl741_5 protein demonstrated at least some similarity to 20 sequences identified as U00027 (Cdc23p cell cycle protein [Saccharomyces cerevisiae]) and U58763 (F10C5.1 [Caenorhabditis elegans]). Based upon sequence similarity, pl741_5 proteins and each similar protein or peptide may share at least some activity. Analysis of the amino acid sequence of the predicted pl741_5 protein reveals the presence of four 25 TPR (tetratricopeptide) domains. TPR domains are found in a wide variety of proteins with varying functions and localizations — from the nucleus to the extracellular milieu — and are thought to function as protein-protein interaction domains. The TPR domains are found at amino acid residues 166-194, 328-356, 362-390, and 396-424 of SEQ ID NO:28.

Clone "pp314_19"

A polynucleotide of the present invention has been identified as clone "pp314_19". pp314_19 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins 5 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pp314_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pp314_19 protein").

The nucleotide sequence of pp314_19 as presently determined is reported in SEQ 10 ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pp314_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 147 to 159 of SEQ ID NO:30 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 160; amino acids 238 to 15 250 of SEQ ID NO:30 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 251. Due to the hydrophobic nature of these possible leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the pp314_19 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone 20 pp314_19 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pp314_19 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pp314_19 demonstrated at least some similarity with sequences identified as AA044042 (zk58g05.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA 25 clone 487064 5', mRNA sequence), AA127902 (zl12d01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 501697 5'), AA609481 (af14a12.s1 Soares testis NHT Homo sapiens cDNA clone 1031614 3', mRNA sequence), T26699 (Human gene signature HUMGS08949; standard; cDNA to mRNA), and W93399 (zd95b06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357203 3'). The predicted amino acid sequence 30 disclosed herein for pp314_19 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pp314_19 protein demonstrated at least some similarity to sequences identified as AE000857 (chaperonin [Methanobacterium thermoautotrophicum]), AJ006549 (ThsA [Pyrodictium occultum]), and L34691 (thermophilic factor 56 [Sulfolobus shibatae]). Based upon sequence

similarity, pp314_19 proteins and each similar protein or peptide may share at least some activity. Analysis of the amino acid sequence of the predicted pp314_19 protein revealed the cpn60_TCP1 signature (at amino acids 29-570 of SEQ ID NO:30) which has some ATPase activity and is indicative of chaperonins. A P-loop motif — a common motif in 5 ATP- and GTP-binding proteins — is found around amino acid 200 of SEQ ID NO:30. The presence of the P-loop is interesting when taken in conjunction with the potential ATPase activity associated with the cpn60_TCP1 signature. The TopPredII computer program predicts three additional potential transmembrane domains within the pp314_19 protein sequence, centered around amino acids 55, 90, and 330 of SEQ ID NO:30, 10 respectively.

pp314_19 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 6 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "pv35_1"

A polynucleotide of the present invention has been identified as clone "pv35_1". pv35_1 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 20 analysis of the amino acid sequence of the encoded protein. pv35_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv35_1 protein").

The nucleotide sequence of pv35_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper 25 reading frame and the predicted amino acid sequence of the pv35_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv35_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pv35_1 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv35_1 demonstrated at least some similarity with sequences identified as AA335869 (EST40348 Epididymus Homo sapiens cDNA 5' end), AA599418 (ag23c03.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1071172 3'), and H03595

(yj42e06.r1 *Homo sapiens* cDNA clone 151426 5'). The predicted amino acid sequence disclosed herein for pv35_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pv35_1 protein demonstrated at least some similarity to sequences identified as Z99277 (Y53C12A.3 5 [Caenorhabditis elegans]). Based upon sequence similarity, pv35_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the pv35_1 protein sequence, centered around amino acids 127, 161, 192, and 250 of SEQ ID NO:32, respectively.

10

Clone "pw337_6"

A polynucleotide of the present invention has been identified as clone "pw337_6". pw337_6 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 15 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw337_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw337_6 protein").

The nucleotide sequence of pw337_6 as presently determined is reported in SEQ 20 ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw337_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Another potential pw337_6 reading frame and predicted amino acid sequence is encoded by basepairs 648 to 908 of SEQ ID NO:33 and is reported in SEQ ID NO:238. The 25 overlapping reading frames of SEQ ID NO:34 and SEQ ID NO:238 could be joined if a frameshift were introduced into the nucleotide sequence of SEQ ID NO:33 between position 645 and position 736.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw337_6 should be approximately 1000 bp.

30 The nucleotide sequence disclosed herein for pw337_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pw337_6 demonstrated at least some similarity with sequences identified as AA682471 (zj18c02.s1 Soares fetal liver spleen 1NFLS S1 *Homo sapiens* cDNA clone 450626 3', mRNA sequence), T20708 (Human gene signature HUMGS01925;

standard; cDNA to mRNA), W24658 (zb63b05.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308241 5'), and Z82192 (Homo sapiens DNA sequence from PAC 186O1 on chromosome 22). The predicted amino acid sequence disclosed herein for pw337_6 was searched against the GenPept and GeneSeq amino acid sequence databases 5 using the BLASTX search protocol. The predicted pw337_6 protein demonstrated at least some similarity to the sequence identified as Z82192 (dJ186O1.1 [Homo sapiens]). Based upon sequence similarity, pw337_6 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pw337_6 protein sequence centered around amino 10 acid 75 of SEQ ID NO:34. The nucleotide sequence of pw337_6 indicates that it may contain one or more repetitive elements.

pw337_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15

Clone "rd610_1"

A polynucleotide of the present invention has been identified as clone "rd610_1". rd610_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 20 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd610_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rd610_1 protein").

The nucleotide sequence of rd610_1 as presently determined is reported in SEQ 25 ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd610_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd610_1 should be approximately 1800 bp.

30 The nucleotide sequence disclosed herein for rd610_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd610_1 demonstrated at least some similarity with sequences identified as AA442056 (zw56f08.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774087 5'), AA992905 (ot92b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens

cDNA clone IMAGE 1624211 3', mRNA sequence), D31767 (Human mRNA for KIAA0058 gene, complete cds), and T40090 (Human Serrate-1 (HJ1) cDNA; standard; cDNA). Based upon sequence similarity, rd610_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential 5 transmembrane domain within the rd610_1 protein sequence centered around amino acid 30 of SEQ ID NO:36; amino acids 23 to 35 of SEQ ID NO:36 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 36.

10 rd610_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 7 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "rd810_6"

15 A polynucleotide of the present invention has been identified as clone "rd810_6". rd810_6 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd810_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to 20 herein as "rd810_6 protein").

The nucleotide sequence of rd810_6 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd810_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino 25 acids 112 to 124 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 125. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rd810_6 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd810_6 should be approximately 850 bp.

The nucleotide sequence disclosed herein for rd810_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd810_6 demonstrated at least some similarity with sequences

identified as AA452718 (zx39d04.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788839 5', mRNA sequence), AA292888 (zt66c01.r1 Soares testis NHT Homo sapiens cDNA clone 727296 5'), and T23348 (Human gene signature HUMGS05169; standard; cDNA to mRNA). Based upon sequence similarity, rd810_6 proteins and each similar 5 protein or peptide may share at least some activity.

rd810_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "cf85_1"

A polynucleotide of the present invention has been identified as clone "cf85_1". A cDNA clone was first isolated from a human adult placenta library cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis 15 of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate cf85_1 from a human adult brain cDNA library. cf85_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cf85_1 protein").

The nucleotide sequence of cf85_1 as presently determined is reported in SEQ ID 20 NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cf85_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cf85_1 should be approximately 2000 bp.

25 The nucleotide sequence disclosed herein for cf85_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cf85_1 demonstrated at least some similarity with sequences identified as H50932 (yo35f03.r1 Homo sapiens cDNA clone 179933 5'), H51595 (yo35f03.s1 Homo sapiens cDNA clone 179933 3'), and T24664 (Human gene signature 30 HUMGS06728; standard; cDNA to mRNA). Based upon sequence similarity, cf85_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the cf85_1 protein sequence, centered around amino acids 150, 195, and 220 of SEQ ID NO:40,

respectively. The nucleotide sequence of cf85_1 indicates that it may contain an Alu repetitive element.

Clone "dd504_18"

5 A polynucleotide of the present invention has been identified as clone "dd504_18". dd504_18 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd504_18 is a full-length
10 clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd504_18 protein").

The nucleotide sequence of dd504_18 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd504_18 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 134 to 146 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 147. Amino acids 7 to 19 of SEQ ID NO:42 are also a possible leader/signal sequence, with a predicted mature amino acid sequence beginning in that case at amino acid 20. Due to the hydrophobic
20 nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the dd504_18 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd504_18 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for dd504_18 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd504_18 demonstrated at least some similarity with sequences identified as AA393779 (zt77f07.r1 Soares testis NHT Homo sapiens cDNA clone 728389 5' similar to WP:F41E7.1 CE03301; mRNA sequence), AA429420 (zw51f02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773595 5' similar to WP W02B12.7 CE03767
30 KINENSIN-LIKE PROTEIN), AC002038 (** SEQUENCING IN PROGRESS *** Human chromosome 16p12 BAC clone CIT987SK-101B6; HTGS phase 1, 1 unordered pieces; Homo sapiens chromosome 2 clone 101B6 from 2p11, complete sequence), H10672 (yl99g09.r1 Homo sapiens cDNA clone 46448 5'), and R59895 (yh07f12.r1 Homo sapiens cDNA clone 42477 5'). The predicted amino acid sequence disclosed herein for dd504_18

was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dd504_18 protein demonstrated at least some similarity to sequences identified as AE000854 (Na+/H+-exchanging protein Na+/H+ antiporter [Methanobacterium thermoautotrophicum]) and Z68106 (F41E7.1 [Caenorhabditis elegans]). Based upon sequence similarity, dd504_18 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eight potential transmembrane domains within the dd504_18 protein sequence, centered around amino acids 20, 48, 118, 144, 191, 220, 268, and 326 of SEQ ID NO:42, respectively.

dd504_18 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 36 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "np26_3"

A polynucleotide of the present invention has been identified as clone "np26_3". np26_3 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. np26_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "np26_3 protein").

The nucleotide sequence of np26_3 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the np26_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone np26_3 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for np26_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. np26_3 demonstrated at least some similarity with sequences identified as AA118527 (mo99d08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 567855 5'), AA284633 (zt15d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713191 3', mRNA sequence), AA427620 (zw30d02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770787 3' similar to contains MER17.b1 MER17

repetitive element; mRNA sequence), and AA496955 (aa42f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 823609 3', mRNA sequence). The predicted amino acid sequence disclosed herein for np26_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted np26_3 5 protein demonstrated at least some similarity to the sequence identified as M86752 (transformation-sensitive protein [Homo sapiens]). Based upon sequence similarity, np26_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the np26_3 protein sequence centered around amino acid 146 of SEQ ID NO:44.

10 np26_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 63 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "pm412_12"

15 A polynucleotide of the present invention has been identified as clone "pm412_12". pm412_12 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm412_12 is a 20 full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm412_12 protein").

25 The nucleotide sequence of pm412_12 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm412_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 607 to 619 of SEQ ID NO:46 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 620. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the pm412_12 30 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm412_12 should be approximately 4000 bp.

The nucleotide sequence disclosed herein for pm412_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. pm412_12 demonstrated at least some similarity with sequences identified as AA176820 (zp34a12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 611326 3'), AA425762 (zw47f10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773227 3' similar to TR:G285999 G285999 ORF, COMPLETE CDS), AA568580 5 (nm21a10.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1060794 similar to TR:G642306 G642306 HYPOTHETICAL 153.8 KD PROTEIN), AA610863 (np98h01.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE 1142449 similar to TR G285999 G285999 ORF, COMPLETE CDS), AA769312 (nz39f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1290179 similar to TR Q15393 Q15393 ORF, COMPLETE 10 CDS; mRNA sequence), D13642 (Human mRNA for KIAA0017 gene, complete cds), and T92977 (ye22e09.r1 Homo sapiens cDNA clone 118504 5'). The predicted amino acid sequence disclosed herein for pm412_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm412_12 protein demonstrated at least some similarity to sequences identified as 15 AF043699 (ORF; similar to human UV-damaged DNA binding factor [C. elegans]), D13642 (KIAA0017 [Homo sapiens]), R72386 (XAP-1, part of the DNA repair complex), and X54413 (alpha1(IX) collagen precursor [Homo sapiens]). Based upon sequence similarity, pm412_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains 20 within the pm412_12 protein sequence, centered around amino acids 277, 415, and 1060 of SEQ ID NO46, respectively.

pm412_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 119 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

25

Clone "pm421_3"

A polynucleotide of the present invention has been identified as clone "pm421_3". pm421_3 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 30 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm421_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm421_3 protein").

The nucleotide sequence of pm421_3 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm421_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 10 to 22 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pm421_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm421_3 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for pm421_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm421_3 demonstrated at least some similarity with sequences identified as AA196485 (zq59a06.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 645874 3'), AA421712 (zu26g11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739172 5', mRNA sequence), AC005026 (Homo sapiens clone GS489L14; HTGS phase 1, 3 unordered pieces), AC005028 (Homo sapiens clone GS539F22; HTGS phase 1, 1 unordered pieces), Q60534 (Human brain Expressed Sequence Tag EST02540; standard; cDNA), and R13985 (yf68h04.r1 Homo sapiens cDNA clone 27722 5'). Based upon sequence similarity, pm421_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the pm421_3 protein sequence centered around amino acid 36 of SEQ ID NO:48.

25

Clone "pv6_1"

A polynucleotide of the present invention has been identified as clone "pv6_1". pv6_1 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or 30 was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pv6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv6_1 protein").

The nucleotide sequence of pv6_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pv6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 39 to 51 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 52. Amino acids 8 to 20 of SEQ ID NO:50 are also a possible leader/signal sequence, with a predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the pv6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv6_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pv6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv6_1 demonstrated at least some similarity with sequences identified as B53192 (CIT-HSP-2009D9.TR CIT-HSP Homo sapiens genomic clone 2009D9, genomic survey sequence), R18429 (yg02g05.r1 Homo sapiens cDNA clone 31056 5'), T77089 (yc93b02.r1 Homo sapiens cDNA clone 23653 5'), and X89480 (S.scrofa mRNA for membrane protein). The predicted amino acid sequence disclosed herein for pv6_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pv6_1 protein demonstrated at least some similarity to the sequence identified as X89480 (transmembrane protein [Sus scrofa]). Based upon sequence similarity, pv6_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pv6_1 protein sequence centered around amino acid 21 of SEQ ID NO:50.

Clone "qs14_3"

A polynucleotide of the present invention has been identified as clone "qs14_3". A cDNA clone was isolated from a human whole embryo cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate qs14_3 from a human fetal heart cDNA library. qs14_3 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "qs14_3 protein").

The nucleotide sequence of qs14_3 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper 5 reading frame and the predicted amino acid sequence of the qs14_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 15 to 27 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should 10 the predicted leader/signal sequence not be separated from the remainder of the qs14_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qs14_3 should be approximately 5000 bp.

The nucleotide sequence disclosed herein for qs14_3 was searched against the 15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qs14_3 demonstrated at least some similarity with sequences identified as AA558554 (nl69g02.s1 NCI_CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE 1045970 similar to TR G307329 G307329 PROTOCADHERIN 43), AB002343 (Human mRNA for KIAA0345 gene), and L43592 (Rattus norvegicus protocadherin-3 (pcdh3) 20 mRNA, and translated products). The predicted amino acid sequence disclosed herein for qs14_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qs14_3 protein demonstrated at least some similarity to sequences identified as AF029343 (protocadherin [Homo sapiens]), AF042192 (protocadherin [Xenopus]), AF052685 (protocadherin 43 [Homo sapiens]), 25 L11373 (protocadherin 43 [Homo sapiens]), R49144 (Product of alternative splicing of human protocadherin-43 mRNA), and Y08715 (protocadherin [Mus musculus]). The cadherins are a family of calcium-binding membrane glycoproteins. Most cadherins are capable of acting as cell adhesion molecules (CAMs). Motif analysis of the predicted qs14_3 protein also detects the 'cadherins extracellular repeated domain signature'. Based 30 upon sequence similarity, qs14_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the qs14_3 protein sequence, one centered around amino acid 510 and another around amino acid 721 of SEQ ID NO:52.

qs14_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 132 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "qy338_9"

A polynucleotide of the present invention has been identified as clone "qy338_9". qy338_9 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on 10 the basis of computer analysis of the amino acid sequence of the encoded protein. qy338_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qy338_9 protein").

The nucleotide sequence of qy338_9 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper 15 reading frame and the predicted amino acid sequence of the qy338_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 144 to 156 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 157. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a 20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qy338_9 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qy338_9 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for qy338_9 was searched against the 25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qy338_9 demonstrated at least some similarity with sequences identified as AA205412 (zq66a09.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 646552 3' similar to contains Alu repetitive element;contains element LTR1 repetitive element; mRNA), AA595068 (no40h10.s1 NCI_CGAP_Pr23 Homo sapiens 30 cDNA clone IMAGE 1103203 similar to WP C27F2.4 CE01171 METHYLTRANSFERASE), AJ224442 (Homo sapiens mRNA for putative methyltransferase), and H40834 (yo05g09.r1 Homo sapiens cDNA clone 177088 5'). The predicted amino acid sequence disclosed herein for qy338_9 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qy338_9 protein

demonstrated at least some similarity to sequences identified as AJ224442 (methyltransferase [Homo sapiens]), U40419 (similar to *S. cerevisiae* gene YCR47C, putative 30.7 kd methyltransferase (SP YCT7_YEAST,P25627) [Caenorhabditis elegans]), and Z69240 (putative methyltransferase [*S. cerevisiae*]). Based upon sequence similarity, qy338_9 5 proteins and each similar protein or peptide may share at least some activity.

qy338_9 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 34 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "rc58_1"

A polynucleotide of the present invention has been identified as clone "rc58_1". rc58_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 15 analysis of the amino acid sequence of the encoded protein. rc58_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rc58_1 protein").

The nucleotide sequence of rc58_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper 20 reading frame and the predicted amino acid sequence of the rc58_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 2 to 14 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should 25 the predicted leader/signal sequence not be separated from the remainder of the rc58_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rc58_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for rc58_1 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rc58_1 demonstrated at least some similarity with sequences identified as AA203670 (zx52d04.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 446119 5' similar to gb X07868_m11 PUTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED (HUMAN); mRNA sequence), AA878778 (oe80h01.s1

NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417969 3', mRNA sequence), and U96448 (Bos taurus cleavage and polyadenylation specificity factor 30 kDa subunit mRNA, complete cds). The predicted amino acid sequence disclosed herein for rc58_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

5 BLASTX search protocol. The predicted rc58_1 protein demonstrated at least some similarity to sequences identified as AF033201 (cleavage and polyadenylation specificity factor [Mus musculus]) and U96448 (cleavage and polyadenylation specificity factor 30 kDa subunit [Bos taurus]). Based upon sequence similarity, rc58_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer

10 program predicts an additional potential transmembrane domain within the rc58_1 protein sequence centered around amino acid 53 of SEQ ID NO:56.

Clone "rd232_5"

A polynucleotide of the present invention has been identified as clone "rd232_5".

15 rd232_5 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd232_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as

20 "rd232_5 protein").

The nucleotide sequence of rd232_5 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd232_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd232_5 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for rd232_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd232_5 demonstrated at least some similarity with sequences

30 identified as AA768103 (oc16g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1341072), AA831487 (oc61a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354172 3', mRNA sequence), and R57296 (F2616 Fetal heart Homo sapiens cDNA clone F2616 5' end). The predicted amino acid sequence disclosed herein for rd232_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted rd232_5 protein demonstrated at least some similarity to the sequence identified as Z79755 (F43G9.2 [Caenorhabditis elegans]). Based upon sequence similarity, rd232_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential 5 transmembrane domain within the rd232_5 protein sequence centered around amino acid 225 of SEQ ID NO:58. The nucleotide sequence of rd232_5 indicates that it may contain a simple AC repeat region.

Clone "ck213_12"

10 A polynucleotide of the present invention has been identified as clone "ck213_12". ck213_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ck213_12 is a full-length 15 clone, including the entire coding sequence of a secreted protein (also referred to herein as "ck213_12 protein").

The nucleotide sequence of ck213_12 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ck213_12 protein 20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ck213_12 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for ck213_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 25 FASTA search protocols. ck213_12 demonstrated at least some similarity with sequences identified as AA062731 (zm01h03.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 512885 3' similar to TR:G1136390 G1136390 KIAA0164 PROTEIN, mRNA sequence), AA173803 (zp30f05.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610977 3', mRNA sequence), D79986 (Human mRNA for KIAA0164 protein 30 gene, complete cds), and R01411 (ye77c11.s1 Homo sapiens cDNA clone 123764 3'). The predicted amino acid sequence disclosed herein for ck213_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ck213_12 protein demonstrated at least some similarity to the sequence identified as D79986 (similar to human DNA-binding protein 5 [Homo sapiens],

KIAA0164 protein [Homo sapiens], HUMKIAA04_1). Based upon sequence similarity, ck213_12 proteins and each similar protein or peptide may share at least some activity.

Clone "pg195_1"

5 A polynucleotide of the present invention has been identified as clone "pg195_1". pg195_1 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pg195_1 is a full-length clone,
10 including the entire coding sequence of a secreted protein (also referred to herein as "pg195_1 protein").

The nucleotide sequence of pg195_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pg195_1 protein
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pg195_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for pg195_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
20 FASTA search protocols. pg195_1 demonstrated at least some similarity with sequences identified as H72617 (yu02g10.r1 Homo sapiens cDNA clone 232674 5') and W37280 (zc11a07.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321972 5', mRNA sequence). The predicted amino acid sequence disclosed herein for pg195_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
25 BLASTX search protocol. The predicted pg195_1 protein demonstrated at least some similarity to the sequence identified as AF007270 (contains similarity to myosin heavy chain [Arabidopsis thaliana]). Based upon sequence similarity, pg195_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the pg195_1 protein
30 sequence, one centered around amino acid 480 and another around amino acid 520 of SEQ ID NO:62. The nucleotide sequence of pg195_1 indicates that it may contain one or more repetitive sequences.

Clone "pw460_5"

A polynucleotide of the present invention has been identified as clone "pw460_5". pw460_5 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw460_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw460_5 protein").

The nucleotide sequence of pw460_5 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw460_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 17 to 29 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pw460_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw460_5 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pw460_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pw460_5 demonstrated at least some similarity with sequences identified as AA447258 (zw93e03.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784540 5', mRNA sequence), AA617801 (nq04f05.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE 1142913), AC002486 (Human BAC clone RG367O17 from 7p15-p21, complete sequence), AC004837 (human genomic DNA fragments), and H45347 (yo65h03.r1 Homo sapiens cDNA clone 182837 5'). Based upon sequence similarity, pw460_5 proteins and each similar protein or peptide may share at least some activity.

30 Clone "qa136_1"

A polynucleotide of the present invention has been identified as clone "qa136_1". qa136_1 was isolated from a human adult cartilage (chondrosarcoma HTB-94 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on

the basis of computer analysis of the amino acid sequence of the encoded protein. qa136_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qa136_1 protein").

The nucleotide sequence of qa136_1 as presently determined is reported in SEQ 5 ID NO:65. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qa136_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 15 to 27 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal 10 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qa136_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qa136_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for qa136_1 was searched against the 15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qa136_1 demonstrated at least some similarity with sequences identified as AA758023 (ah67g02.s1 Soares testis NHT Homo sapiens cDNA clone 1320722 3', mRNA sequence), R69911 (yi47c02.r1 Homo sapiens cDNA clone 142370 5'), and T21835 (Human gene signature HUMGS03376; standard; cDNA to mRNA). Based upon 20 sequence similarity, qa136_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the qa136_1 protein sequence, centered around amino acids 59, 136, 171, 201, and 268 of SEQ ID NO:66, respectively.

qa136_1 protein was expressed in a COS cell expression system, and an expressed 25 protein band of approximately 24 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "qy1261_2"

A polynucleotide of the present invention has been identified as clone "qy1261_2". 30 qy1261_2 was isolated from a human adult blood (promyelocytic Leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.

qy1261_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qy1261_2 protein").

The nucleotide sequence of qy1261_2 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qy1261_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 100 to 112 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 113. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qy1261_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qy1261_2 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for qy1261_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qy1261_2 demonstrated at least some similarity with sequences identified as AA076472 (zm91b06.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545267 5'), AA115700 (zl87g10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 511650 5', mRNA sequence), and AA190522 (zp85e07.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 627012 5'). The predicted amino acid sequence disclosed herein for qy1261_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qy1261_2 protein demonstrated at least some similarity to the sequence identified as U49082 (transporter protein [Homo sapiens]). Based upon sequence similarity, qy1261_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts ten additional potential transmembrane domains within the qy1261_2 protein sequence, centered around amino acids 80, 157, 203, 227, 286, 322, 365, 403, 426, and 462 of SEQ ID NO:68. The nucleotide sequence of qy1261_2 indicates that it may contain one or more Alu repeat sequences.

30

Clone "rd432_4"

A polynucleotide of the present invention has been identified as clone "rd432_4". rd432_4 was isolated from a human kidney (293 embryonal carcinoma cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S.

Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rd432_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rd432_4 protein").

5 The nucleotide sequence of rd432_4 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rd432_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rd432_4 should be approximately 2200 bp.

15 The nucleotide sequence disclosed herein for rd432_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rd432_4 demonstrated at least some similarity with sequences identified as AA662913 (nu92b03.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218125, mRNA sequence). Based upon sequence similarity, rd432_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the rd432_4 protein sequence, which includes amino acids 102-122 of SEQ ID NO:70. The nucleotide sequence of rd432_4 indicates that it may contain one or more Alu repetitive elements.

20 rd432_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "rb789_14"

25 A polynucleotide of the present invention has been identified as clone "rb789_14". rb789_14 was isolated from a human kidney (293 embryonal carcinoma line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rb789_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rb789_14 protein").

The nucleotide sequence of rb789_14 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rb789_14 protein

corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72. Amino acids 9 to 21 of SEQ ID NO:72 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

5 should the predicted leader/signal sequence not be separated from the remainder of the rb789_14 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rb789_14 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for rb789_14 was searched against the

10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rb789_14 demonstrated at least some similarity with sequences identified as AL008582 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223H9; HTGS phase 1), AL022393 (Homo sapiens DNA sequence from P1 p373c6 on chromosome 6p21.31-21.33. Contains zinc finger proteins, pseudogenes, ESTs

15 and STS), N28823 (yx71f11.r1 Homo sapiens cDNA clone 267213 5'), and Q60944 (Human brain Expressed Sequence Tag EST01025; standard; DNA). Based upon sequence similarity, rb789_14 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the rb789_14 protein sequence, one centered around

20 amino acid 30 and another around amino acid 75 of SEQ ID NO:72.

Clone "yd137_1"

A polynucleotide of the present invention has been identified as clone "yd137_1". yd137_1 was isolated from a human adult brain cDNA library and was identified as

25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd137_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd137_1 protein").

The nucleotide sequence of yd137_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper

30 reading frame and the predicted amino acid sequence of the yd137_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 27 to 39 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

should the predicted leader/signal sequence not be separated from the remainder of the yd137_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd137_1 should be approximately 789 bp.

5 The nucleotide sequence disclosed herein for yd137_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yd137_1 demonstrated at least some similarity with sequences identified as AJ015619 (ov29g02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638770 3' similar to WP:C34B2.10 CE16898; mRNA sequence). The predicted
10 amino acid sequence disclosed herein for yd137_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yd137_1 protein demonstrated at least some similarity to the sequence identified as AF043693 (Caenorhabditis elegans cosmid C34B2). Based upon sequence similarity, yd137_1 proteins and each similar protein or peptide may share at least some
15 activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yd137_1 protein sequence, one centered around amino acid 30 and another around amino acid 55 of SEQ ID NO:74.

Clone "yd218_1"

20 A polynucleotide of the present invention has been identified as clone "yd218_1". yd218_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yd218_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yd218_1 protein").
25 The nucleotide sequence of yd218_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yd218_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 2 to 14 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted
30 mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yd218_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yd218_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for yd218_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 5 FASTA search protocols. yd218_1 demonstrated at least some similarity with sequences identified as AA402818 (zu55f06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741923 3', mRNA sequence) and AI150344 (qf35b11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751997 3', mRNA sequence). Based upon sequence similarity, yd218_1 proteins and each similar protein or peptide may share at least some 10 activity. The TopPredII computer program predicts two additional potential transmembrane domains within the yd218_1 protein sequence, one centered around amino acid 66 and another around amino acid 100 of SEQ ID NO:76.

yd218_1 protein was expressed in a COS cell expression system, and an expressed 15 protein band of approximately 15 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ye11_1"

A polynucleotide of the present invention has been identified as clone "ye11_1". ye11_1 was isolated from a humna fetal brain cDNA library and was identified as 20 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye11_1 protein").

The nucleotide sequence of ye11_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper 25 reading frame and the predicted amino acid sequence of the ye11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye11_1 should be approximately 2700 bp.

The nucleotide sequence disclosed herein for ye11_1 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye11_1 demonstrated at least some similarity with sequences identified as AC005082 (** SEQUENCING IN PROGRESS *** Homo sapiens clone RG271G13; HTGS phase 1, 7 unordered pieces). The predicted amino acid sequence disclosed herein for ye11_1 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted ye11_1 protein demonstrated at least some similarity to sequences identified as AF059569 (actin binding protein MAYVEN [Homo sapiens]) and R94386 (Human neural cell protein marker RR/B). MAYVEN is an actin-binding protein expressed in brain. Hidden markov model 5 analysis reveals the presence of a BTB (BR-c/Ttk) domain in the predicted ye11_1 protein. BTB domains are characteristic of certain bacterial membrane transport proteins. The MAYVEN protein is thought to contain a similar BTB motif, an indication that ye11_1 and MAYVEN may share a similar function. Based upon sequence similarity, ye11_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII 10 computer program predicts two potential transmembrane domains within the ye11_1 protein sequence, one centered around amino acid 20 and another around amino acid 480 of SEQ ID NO:78.

ye11_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 57 kDa was detected in conditioned medium and 15 membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ye72_1"

A polynucleotide of the present invention has been identified as clone "ye72_1". ye72_1 was isolated from a human fetal brain cDNA library and was identified as 20 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye72_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye72_1 protein").

The nucleotide sequence of ye72_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper 25 reading frame and the predicted amino acid sequence of the ye72_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 24 to 36 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should 30 the predicted leader/signal sequence not be separated from the remainder of the ye72_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye72_1 should be approximately 2261 bp.

The nucleotide sequence disclosed herein for ye72_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye72_1 demonstrated at least some similarity with sequences identified as AA968450 (op49d06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone 5 IMAGE:1580171 3', mRNA sequence). The predicted amino acid sequence disclosed herein for ye72_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ye72_1 protein demonstrated at least some similarity to sequences identified as U16258 (I kappa BR [Homo sapiens]) and W15483 (Human P28). Based upon sequence similarity, ye72_1 proteins and each 10 similar protein or peptide may share at least some activity. Hidden markov model analysis reveals the presence of three ankyrin repeats in the predicted ye72_1 protein at amino acids 273 to 306, 307 to 339, and 341 to 373 of SEQ ID NO:80. The ankyrin 33-residue repeating motif, an L-shaped structure with protruding beta-hairpin tips, mediates specific macromolecular interactions with cytoskeletal, membrane, and regulatory proteins. The 15 TopPredII computer program predicts an additional potential transmembrane domain within the ye72_1 protein sequence centered around amino acid 140 of SEQ ID NO:80.

Clone "ye78_1"

A polynucleotide of the present invention has been identified as clone "ye78_1". 20 ye78_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye78_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye78_1 protein").

The nucleotide sequence of ye78_1 as presently determined is reported in SEQ ID 25 NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ye78_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 78 to 90 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 91. Amino acids 42 to 54 are also a possible 30 leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 55. Due to the hydrophobic nature of leader/signal sequences, both of these predicted and possible leader sequences are likely to act as a transmembrane domain should either of them not be separated from the remainder of the ye78_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye78_1 should be approximately 2654 bp.

The nucleotide sequence disclosed herein for ye78_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 5 FASTA search protocols. ye78_1 demonstrated at least some similarity with sequences identified as AA522797 (ni40c10.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:979314, mRNA sequence). Based upon sequence similarity, ye78_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the ye78_1 protein 10 sequence, centered around amino acids 55, 75, 84, and 480 of SEQ ID NO:12, respectively.

Clone "ye90_1"

A polynucleotide of the present invention has been identified as clone "ye90_1". ye90_1 was isolated from a human fetal brain cDNA library and was identified as 15 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ye90_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ye90_1 protein").

The nucleotide sequence of ye90_1 as presently determined is reported in SEQ ID NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper 20 reading frame and the predicted amino acid sequence of the ye90_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 7 to 19 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should 25 the predicted leader/signal sequence not be separated from the remainder of the ye90_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ye90_1 should be approximately 1505 bp.

The nucleotide sequence disclosed herein for ye90_1 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ye90_1 demonstrated at least some similarity with sequences identified as AI079268 (oz32f06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1677059 3', mRNA sequence) and T25543 (Human gene signature HUMGS07715, standard; cDNA to mRNA). Based upon sequence similarity, ye90_1

proteins and each similar protein or peptide may share at least some activity. Motifs analysis reveals the presence of a neutral zinc metallopeptidases, zinc-binding region signature beginning around amino acid residue 236 of SEQ ID NO:84; some known secreted proteins have this motif. The TopPredII computer program predicts two 5 additional potential transmembrane domains within the ye90_1 protein sequence, one centred around amino acid 195 and another around amino acid 300 of SEQ ID NO:84.

Clone "yi62_1"

A polynucleotide of the present invention has been identified as clone "yi62_1".
10 yi62_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yi62_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "yi62_1 protein").

The nucleotide sequence of yi62_1 as presently determined is reported in SEQ ID
15 NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yi62_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 2 to 14 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal
20 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yi62_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yi62_1 should be approximately 1240 bp.

The nucleotide sequence disclosed herein for yi62_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. yi62_1 demonstrated at least some similarity with sequences identified as R57572 (F3589 Fetal heart Homo sapiens cDNA clone F3589 5' end, mRNA sequence). Based upon sequence similarity, yi62_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four
30 potential transmembrane domains within the yi62_1 protein sequence, centered around amino acids 15, 75, 100, and 125 of SEQ ID NO:86, respectively.

Clone "yk78_1"

A polynucleotide of the present invention has been identified as clone "yk78_1".
yk78_1 was isolated from a human adult thymus cDNA library and was identified as
encoding a secreted or transmembrane protein on the basis of computer analysis of the
5 amino acid sequence of the encoded protein. yk78_1 is a full-length clone, including the
entire coding sequence of a secreted protein (also referred to herein as "yk78_1 protein").

The nucleotide sequence of yk78_1 as presently determined is reported in SEQ ID
NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper
reading frame and the predicted amino acid sequence of the yk78_1 protein
10 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino
acids 57 to 69 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted
mature amino acid sequence beginning at amino acid 70. Amino acids 7 to 19 are a
possible leader/signal sequence, with the predicted mature amino acid sequence
beginning at amino acid 20. Due to the hydrophobic nature of leader/signal sequences,
15 both of these predicted and possible leader sequences are likely to act as a transmembrane
domain should either of them not be separated from the remainder of the yk78_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
yk78_1 should be approximately 1088 bp.

The nucleotide sequence disclosed herein for yk78_1 was searched against the
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
FASTA search protocols. yk78_1 demonstrated at least some similarity with sequences
identified as AC004921 (** SEQUENCING IN PROGRESS ** Homo sapiens clone
DJ0899E09; HTGS phase 1, 11 unordered pieces). Based upon sequence similarity, yk78_1
proteins and each similar protein or peptide may share at least some activity. The
25 TopPredII computer program predicts two potential transmembrane domains within the
yk78_1 protein sequence, one centered around amino acid 20 and another around amino
acids 60 of SEQ ID NO:88.

Clone "yk251_1"

30 A polynucleotide of the present invention has been identified as clone "yk251_1".
yk251_1 was isolated from a human adult thymus cDNA library and was identified as
encoding a secreted or transmembrane protein on the basis of computer analysis of the
amino acid sequence of the encoded protein. yk251_1 is a full-length clone, including the
entire coding sequence of a secreted protein (also referred to herein as "yk251_1 protein").

The nucleotide sequence of yk251_1 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yk251_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 17 to 29 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk251_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yk251_1 should be approximately 2558 bp.

15 The nucleotide sequence disclosed herein for yk251_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the databases. The TopPredII computer program predicts a potential transmembrane domain within the yk251_1 protein sequence centered, around amino acid 20 of SEQ ID NO:90. The nucleotide sequence of yk251_1 indicates that it may contain Alu and SVA repetitive elements.

Clone "yt14_1"

20 A polynucleotide of the present invention has been identified as clone "yt14_1". yt14_1 was isolated from a human adult retina (WERI-Rb1 retinoblastoma line) cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. yt14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to 25 herein as "yt14_1 protein").

25 The nucleotide sequence of yt14_1 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the yt14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 1 to 9 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 10. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the yk251_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone yt14_1 should be approximately 2429 bp.

The nucleotide sequence disclosed herein for yt14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 5 FASTA search protocols. yt14_1 demonstrated at least some similarity with sequences identified as W07167 (za93b12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 300095 5', mRNA sequence). The predicted amino acid sequence disclosed herein for yt14_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted yt14_1 protein demonstrated at least 10 some similarity to the sequence identified as AF002196 (weak similarity to *Bacillus* and *Pseudomonas* probable glucarate transporters (GI 709999 and PIR S27616) [Caenorhabditis elegans]). Based upon sequence similarity, yt14_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the yt14_1 protein 15 sequence, centered around amino acids 10, 40, 65, 90, 130, and 160 of SEQ ID NO:92, respectively. The nucleotide sequence of yt14_1 indicates that it may contain Alu and L1 repetitive elements.

Clone "bf157_16"

20 A polynucleotide of the present invention has been identified as clone "bf157_16". bf157_16 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bf157_16 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bf157_16 protein").

25 The nucleotide sequence of bf157_16 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bf157_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone 30 bf157_16 should be approximately 3480 bp.

The nucleotide sequence disclosed herein for bf157_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf157_16 demonstrated at least some similarity with sequences identified as AA186595 (zo71g04.r1 Stratagene pancreas (#937208) Homo sapiens cDNA

clone 592374 5' similar to WP C16A3.3 CE04004 HUMAN ALPHA-FETOPROTEIN ENHANCER-BINDING PROTEIN), AA630405 (ac09b05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 855921 3' similar to WP C16A3.3 CE04004 HUMAN ALPHA-FETOPROTEIN ENHANCER-BINDING PROTEIN; mRNA sequence), AF075104

5 (Homo sapiens full length insert cDNA YR39H06), H49655 (yq20h07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274428 3'), Z28494 (H. sapiens partial cDNA sequence; clone 22G07; version 1; strand(-), single read), Z56794 (H.sapiens CpG island DNA genomic Mse1 fragment, clone), and Z64553 (H.sapiens CpG island DNA genomic Mse1 fragment, clone 139f5, forward read cpg139f5.ft1a). The predicted amino acid

10 sequence disclosed herein for bf157_16 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bf157_16 protein demonstrated at least some similarity to sequences identified as R23962 (AFP-1. DNA encoding protein binding to alpha-fetoprotein gene enhancer -useful for prodn. of biological active protein), and U41534 (similar to yeast hypothetical protein

15 (SP:YB9M_YEAST,P38344); similar to human alpha-fetoprotein enhancer-binding protein (PIR:A41948) [Caenorhabditis elegans]). Based upon sequence similarity, bf157_16 proteins and each similar protein or peptide may share at least some activity. Hidden Markov model and motifs analyses have revealed the presence of the following protein domains in the predicted bf157_16 protein: four Zinc finger, C2H2 type, domains at

20 amino acids 4 to 28, 67 to 91, 252 to 275, and 303 to 330 of SEQ ID NO:94; and a D-isomer-specific 2-hydroxyacid dehydrogenases signature at residues 119 to 131 of SEQ ID NO:94. A number of NAD-dependent 2-hydroxyacid dehydrogenases, with at least some specificity for the D-isomer of their substrate, have been shown to be functionally and structurally related. Clone bf157_16 appears to encode a novel protein which may have

25 NAD-dependent 2-hydroxyacid dehydrogenase activity.

bf157_16 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

30 Clone "bk343_2"

A polynucleotide of the present invention has been identified as clone "bk343_2". bk343_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer

analysis of the amino acid sequence of the encoded protein. bk343_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bk343_2 protein").

The nucleotide sequence of bk343_2 as presently determined is reported in SEQ 5 ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bk343_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

Another possible reading frame within the bk343_2 clone extends from nucleotide 45 to nucleotide 188 of SEQ ID NO:95, and encodes the amino acid sequence reported in 10 SEQ ID NO:239. Amino acids 5 to 17 of SEQ ID NO:239 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:239.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bk343_2 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for bk343_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bk343_2 demonstrated at least some similarity with sequences 20 identified as AA156969 (zo51d05.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 590409 5'), AA947938 (oe60c08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416014 3', mRNA sequence), N31147 (yx52g05.r1 Homo sapiens cDNA clone 265400 5'), N42759 (yy22a09.r1 Homo sapiens cDNA clone 271960 5'), N47537 (yy90h10.s1 Homo sapiens cDNA clone 280867 3'), R68913 (yi43b04.r1 Homo sapiens 25 cDNA clone 141967 5'), T24885 (Human gene signature HUMGS06991; standard; cDNA to mRNA), and T30099 (EST112339 Homo sapiens cDNA 5' end similar to None). The predicted amino acid sequence disclosed herein for bk343_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bk343_2 protein demonstrated at least some similarity to sequences 30 identified as Z72508 (F28H7.4 [Caenorhabditis elegans]) and Z78417 (C35C5.3 [Caenorhabditis elegans]). Based upon sequence similarity, bk343_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the bk343_2 protein sequence centered around amino acid 36 of SEQ ID NO:96.

Clone "cd205_2"

A polynucleotide of the present invention has been identified as clone "cd205_2". cd205_2 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of 5 the encoded protein. cd205_2 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "cd205_2 protein").

The nucleotide sequence of cd205_2 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cd205_2 protein 10 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino acids 92 to 104 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 105. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated 15 from the remainder of the cd205_2 protein.

Another possible reading frame within the cd205_2 clone extends from nucleotide 59 to nucleotide 478 of SEQ ID NO:97, and encodes the amino acid sequence reported in SEQ ID NO:240. The open reading frames encoding the amino acid sequences of SEQ ID NO:98 and SEQ ID NO:240 could be joined if one or more frame shifts were made in the 20 nucleotide sequence of SEQ ID NO:97.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cd205_2 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for cd205_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 25 FASTA search protocols. cd205_2 demonstrated at least some similarity with sequences identified as AA053543 (zl71f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 510091 5' similar to gb:M77830 DESMOPLAKIN I AND II (HUMAN)), AC005332 (Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence), N84944 (J1677F 30 Homo sapiens cDNA clone J1677 5' similar to CHROMOSOME 4 (CLONE P4-661) STS4-563), N86274 (J7481F Fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7481 5' similar to CHROMOSOME 4 (CLONE P4-661) STS4-563), W68823 (zd37f04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342847 5', mRNA sequence), and Z54387 (H.sapiens CpG island DNA genomic Mse1 fragment, clone 10g3, reverse read cpg10g3.rt1a). Based upon sequence similarity, cd205_2 proteins and each similar protein

or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cd205_2 protein sequence located around amino acid 105 of SEQ ID NO:98.

5 Clone "cw1292_8"

A polynucleotide of the present invention has been identified as clone "cw1292_8". cw1292_8 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 10 analysis of the amino acid sequence of the encoded protein. cw1292_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1292_8 protein").

The nucleotide sequence of cw1292_8 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper 15 reading frame and the predicted amino acid sequence of the cw1292_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 18 to 30 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a 20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1292_8 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1292_8 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for cw1292_8 was searched against the 25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1292_8 demonstrated at least some similarity with sequences identified as AA017976 (mh46h10.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus), AA423855 (zv79c04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759846 3'), AA626784 (ad09f08.s1 Soares NbHFB Homo sapiens cDNA clone 877767 3', mRNA 30 sequence), H23387 (ym57f05.r1 Homo sapiens cDNA clone 52337 5'), H78534 (yu13d06.r1 Homo sapiens cDNA clone 233675 5'), H79021 (yu13d06.s1 Homo sapiens cDNA clone 233675 3'), R44807 (yg23g06.s1 Homo sapiens cDNA clone 33217 3'), T24772 (Human gene signature HUMGS06848; standard; cDNA to mRNA), T97424 (ye53h08.r1 Homo sapiens cDNA clone 121503 5'); and Z44597 (H. sapiens partial cDNA sequence; clone c-25a05).

The predicted amino acid sequence disclosed herein for cw1292_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1292_8 protein demonstrated at least some similarity to the sequence identified as M33521 (HLA-B-associated transcript 3 (BAT3) [Homo]). Based 5 upon sequence similarity, cw1292_8 proteins and each similar protein or peptide may share at least some activity.

Clone "cw1475_2"

A polynucleotide of the present invention has been identified as clone "cw1475_2".
10 cw1475_2 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1475_2 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "cw1475_2 protein").

The nucleotide sequence of cw1475_2 as presently determined is reported in SEQ 15 ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1475_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1475_2 should be approximately 2800 bp.

20 The nucleotide sequence disclosed herein for cw1475_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1475_2 demonstrated at least some similarity with sequences identified as AA527429 (ng41a10.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937338, mRNA sequence), AD000092 (Homo sapiens DNA from chromosome 25 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence), H98508 (yv90f08.r1 Homo sapiens cDNA clone 250023 5'), N25554 (yx76f08.s1 Homo sapiens cDNA clone 267687 3'), N50970 (yy94b06.s1 Homo sapiens cDNA clone 281171 3'), N81188 (yw36g06.r1 Homo sapiens cDNA clone 254362 5'), R32569 (yh54g03.r1 Homo sapiens cDNA clone 133588 5'), R81017 (yi94g02.r1 30 Homo sapiens cDNA clone 146930 5' similar to contains Alu repetitive element;contains MER30 repetitive element), T06537 (EST04426 Homo sapiens cDNA clone HFBDU83 similar to EST containing Alu repeat), T31594 (Probe (BLUR11) for Alu repeat sequence), and W30895 (zb78e12.r1 Soares senescent fibroblasts NbHSF Homo). Based upon sequence similarity, cw1475_2 proteins and each similar protein or peptide may share at

least some activity. The nucleotide sequence of cw1475_2 indicates that it may contain one or more of the following repetitive elements: Alu, SVA.

Clone "dd428_4"

5 A polynucleotide of the present invention has been identified as clone "dd428_4". dd428_4 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd428_4 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "dd428_4 protein").

10 The nucleotide sequence of dd428_4 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd428_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd428_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for dd428_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd428_4 demonstrated at least some similarity with sequences identified as AC000057 (Human BAC clone RG067M09 from 7q21-7q22; HTGS phase 3, 20 complete sequence), AC005500 (complete sequence), L27428 (Human L1 putative reverse transcriptase gene insertion in hamster, 3'end), T86176 (yd78c11.s1 Homo sapiens cDNA clone 114356 3' similar to gb L25879 EPOXIDE HYDROLASE (HUMAN); contains L1 repetitive element), X61307 (Staphylococcus aureus spa gene for protein A), and Z69647 (Human DNA sequence from cosmid E118G4, maps to 10cen and 11q13-q14). Based upon 25 sequence similarity, dd428_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dd428_4 indicates that it may contain L1 repeat sequences.

Clone "dh1073_12"

30 A polynucleotide of the present invention has been identified as clone "dh1073_12". dh1073_12 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dh1073_12 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "dh1073_12 protein").

The nucleotide sequence of dh1073_12 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dh1073_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dh1073_12 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for dh1073_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dh1073_12 demonstrated at least some similarity with sequences 10 identified as AA257983 (zs35h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 687221 3' similar to TR G666014 G666014 SA SA GENE PRODUCT, COMPLETE CDS PRECURSOR; mRNA sequence), AA526325 (ni59g06.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone 981178 similar to contains Alu repetitive element), AF001549 (Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence), N57823 (yv59e04.s1 15 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 247038 3'), and N68408 (za13c05.s1 Homo sapiens cDNA clone 292424 3'). The predicted amino acid sequence disclosed herein for cw1292_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dh1073_12 protein demonstrated at least some similarity to the sequence identified as AC003034 (Gene with 20 similarity to rat kidney-specific (KS) gene [Homo sapiens]). Based upon sequence similarity, dh1073_12 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dh1073_12 indicates that it may contain an Alu repetitive element.

25 Clone "dw78_1"

A polynucleotide of the present invention has been identified as clone "dw78_1". dw78_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 30 analysis of the amino acid sequence of the encoded protein. dw78_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dw78_1 protein").

The nucleotide sequence of dw78_1 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the dw78_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dw78_1 should be approximately 1400 bp.

5 The nucleotide sequence disclosed herein for dw78_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dw78_1 demonstrated at least some similarity with sequences identified as AA807622 (nv65g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1234724, mRNA sequence), AF086326 (Homo sapiens full length insert cDNA 10 clone ZD54A02), D37980 (Dictyostelium discoidium DDCOF1 gene for cofilin, complete cds (exon1-2)), H26207 (yl53c04.r1 Homo sapiens cDNA clone 161958 5'), N72717 (za47h03.s1 Homo sapiens cDNA clone 295733 3' similar to contains Alu repetitive element;contains element L1 repetitive element), T23963 (Human gene signature HUMGS05917; standard; cDNA to mRNA), U14567 (***ALU WARNING Human Alu-J 15 subfamily consensus sequence), U43572 (Human alpha-N-acetylglucosaminidase (NAGLU) gene, complete cds), W42787 (zc25a04.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323310 3'), and W73472 (zd54a02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344426 3', mRNA sequence). The predicted amino acid sequence disclosed herein for dw78_1 was searched against the GenPept and 20 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dw78_1 protein demonstrated at least some similarity to the sequence identified as D32202 (alpha 1C adrenergic receptor isoform 2 [Homo sapiens]). Based upon sequence similarity, dw78_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential 25 transmembrane domains within the dw78_1 protein sequence, one centered around amino acid 45 and another around amino acid 93 of SEQ ID NO:108. The nucleotide sequence of dw78_1 indicates that it may contain an Alu repetitive element.

Clone "fh116_11"

30 A polynucleotide of the present invention has been identified as clone "fh116_11". fh116_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh116_11 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "fh116_11 protein").

The nucleotide sequence of fh116_11 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper 5 reading frame and the predicted amino acid sequence of the fh116_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh116_11 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for fh116_11 was searched against the 10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh116_11 demonstrated at least some similarity with sequences identified as AA054185 (zf51c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone 380458 5'), AA057975 (mj57b02.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 480171 5' similar to WP:F57A8.2 CE05983), AA128902 (zn90a05.s1 Stratagene 15 lung carcinoma 937218 Homo sapiens cDNA clone 565424 3'), AA426021 (zw49h09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773441 3'), AA505926 (rh98g03.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone 966580), AI079540 (oz04e08.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674374 3' similar to WP:F57A8.2 CE05983; mRNA sequence), H68794 (yr91h09.s1 Homo sapiens 20 cDNA clone 212705 3'), H86659 (yt02c04.r1 Homo sapiens cDNA clone 223110 5'), T24554 (Human gene signature HUMGS06604; standard; cDNA to mRNA), U96490 (Rattus norvegicus liver mRNA, complete cds), and W00635 (yy71d12.r1 Homo sapiens cDNA clone 278999 5' similar to contains element PTR5 repetitive element). The predicted amino acid sequence disclosed herein for fh116_11 was searched against the GenPept and 25 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fh116_11 protein demonstrated at least some similarity to sequences identified as AF004876 (54TMp [Homo sapiens]), U96490 (unknown [Rattus norvegicus]), and Z70781 (F57A8.2 [Caenorhabditis elegans]). Based upon sequence similarity, fh116_11 proteins and each similar protein or peptide may share at least some activity. The 30 TopPredII computer program predicts five potential transmembrane domains within the fh116_11 protein sequence, centered around amino acids 35 to 49, 136, 171, 215, and 270 of SEQ ID NO:110, respectively.

fh116_11 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 28 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5 Clone "fy356_14"

A polynucleotide of the present invention has been identified as clone "fy356_14". fy356_14 was isolated from a human fetal placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 10 analysis of the amino acid sequence of the encoded protein. fy356_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fy356_14 protein").

The nucleotide sequence of fy356_14 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper 15 reading frame and the predicted amino acid sequence of the fy356_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 385 to 397 of SEQ ID NO:112 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 398. Due to the hydrophobic nature of this possible leader/signal sequence, it is likely to act as a 20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fy356_14 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fy356_14 should be approximately 3700 bp.

The nucleotide sequence disclosed herein for fy356_14 was searched against the 25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fy356_14 demonstrated at least some similarity with sequences identified as AA017639 (ze38c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone 361256 5' similar to PIR S55385 S55385 PEA-15 protein - mouse), AA181529 (zp51f07.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 612997 3'), AA687129 30 (nv63d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1234469), AA811277 (ob68e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336546, mRNA sequence), N53623 (yz04e01.r1 Homo sapiens cDNA clone 282072 5'), T25935 (Human gene signature HUMGS08167; standard; cDNA to mRNA), T24538 (Human gene signature HUMGS06585; standard; cDNA to mRNA), and X86809 (H.sapiens mRNA for

major astrocytic phosphoprotein PEA-15). The predicted amino acid sequence disclosed herein for fy356_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fy356_14 protein demonstrated at least some similarity to the sequence identified as X86809 (PEA-15 gene 5 product [Homo sapiens]). Based upon sequence similarity, fy356_14 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the fy356_14 protein sequence, centered around amino acid 398 of SEQ ID NO:112.

10 Clone "iw66_1"

A polynucleotide of the present invention has been identified as clone "iw66_1". iw66_1 was isolated from a human adult retina (WERI-Rb1 retinoblastoma line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on 15 the basis of computer analysis of the amino acid sequence of the encoded protein. iw66_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "iw66_1 protein").

The nucleotide sequence of iw66_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper 20 reading frame and the predicted amino acid sequence of the iw66_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 9 to 21 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a 25 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the iw66_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone iw66_1 should be approximately 1450 bp.

The nucleotide sequence disclosed herein for iw66_1 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. iw66_1 demonstrated at least some similarity with sequences identified as AA216917 (mv75h11.r1 Soares mouse 3'NME12 5' Mus musculus cDNA clone 660933 5'), AA339406 (EST44484 Fetal brain I Homo sapiens cDNA 5' end), AI275861 (ql68b12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877471 3', mRNA

sequence), Q61257 (Human brain Expressed Sequence Tag EST01278; standard; DNA), R89651 (ym97c08.r1 Homo sapiens cDNA clone 166862 5'), W53584 (md55f06.r1 Soares mouse embryc NbME13.5 14.5 Mus musculus cDNA clone 372323 5'), and Z60886 (H.sapiens CpG island DNA genomic Mse1 fragment, clone 38a8, reverse read 5 cpg38a8.rt1a). The predicted amino acid sequence disclosed herein for iw66_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted iw66_1 protein demonstrated at least some similarity to sequences identified as AF004874 (latent TGF-beta binding protein-2 [Mus musculus]), L29029 (amino acid feature Rod protein domain, aa 266 468; amino acid 10 feature globular protein domain, aa 32 .. 265 [Chlamydomonas reinhardtii]), R27150 (PspA fragment), and R79478 (Mouse LTBP-2). Based upon sequence similarity, iw66_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the iw66_1 protein sequence, centered around amino acids 45, 74, and 158 of SEQ ID NO:114, 15 respectively. The nucleotide sequence of iw66_1 indicates that it may contain one or more of the following repetitive elements: MIR.

Clone "kh13_4"

A polynucleotide of the present invention has been identified as clone "kh13_4". 20 kh13_4 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. kh13_4 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "kh13_4 protein").

The nucleotide sequence of kh13_4 as presently determined is reported in SEQ ID 25 NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the kh13_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kh13_4 should be approximately 950 bp.

30 The nucleotide sequence disclosed herein for kh13_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kh13_4 demonstrated at least some similarity with sequences identified as AA435981 (zu01f08.s1 Soares testis NHT Homo sapiens cDNA clone 730599 3'), AA436078 (zu01f08.r1 Soares testis NHT Homo sapiens cDNA clone 730599 5'),

AA778636 (af87c04.s1 Soares testis NHT Homo sapiens cDNA clone 1048998 3' similar to gb:M94856 PSORIASIS-ASSOCIATED FATTY ACID BINDING PROTEIN HOMOLOG (HUMAN); mRNA sequence), M94856 (Human fatty acid binding protein homologue (PA-FABP) mRNA, complete cds), and Q66842 (Melanogenic inhibitor; standard; DNA).

5 The predicted amino acid sequence disclosed herein for kh13_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted kh13_4 protein demonstrated at least some similarity to sequences identified as M94856 (fatty acid binding protein homologue [Homo sapiens]) and R55866 (Melanogenic inhibitor). Fatty acid binding protein homologue (M94856) is described as

10 "a novel keratinocyte protein (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is highly up-regulated in psoriatic skin and that shares similarity to fatty acid-binding proteins." Based upon sequence similarity, kh13_4 proteins and each similar protein or peptide may share at least some activity.

15 Clone "ko258_4"

A polynucleotide of the present invention has been identified as clone "ko258_4". ko258_4 was isolated from a human adult uterus cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ko258_4 is a full-length clone, including the entire coding sequence 20 of a novel protein (also referred to herein as "ko258_4 protein").

The nucleotide sequence of ko258_4 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ko258_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ko258_4 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for ko258_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ko258_4 demonstrated at least some similarity with sequences 30 identified as AC002401 (**SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone RPC875H18; HTGS phase 1, 4 unordered pieces), AC002401 (Homo sapiens chromosome 17, clone RPC875H18, complete sequence), C15329 (Human fetal brain cDNA 5'-end GEN-133H10, mRNA sequence), AF035306 (Homo sapiens clone 23771 mRNA sequence), and R28382 (IMAGE 3p clone). Based upon sequence similarity,

ko258_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the ko258_4 protein sequence, centered around amino acid 28 of SEQ ID NO:118.

5 Clone "kv10_8"

A polynucleotide of the present invention has been identified as clone "kv10_8". kv10_8 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 10 analysis of the amino acid sequence of the encoded protein. kv10_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "kv10_8 protein").

The nucleotide sequence of kv10_8 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper 15 reading frame and the predicted amino acid sequence of the kv10_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kv10_8 should be approximately 4300 bp.

The nucleotide sequence disclosed herein for kv10_8 was searched against the 20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kv10_8 demonstrated at least some similarity with sequences identified as AA418842 (zw01e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 768046 3'), AC004228 (**SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12 pac pDJ519o3; HTGS phase 1, 18 unordered pieces), AF052108 (Homo sapiens clone 25 23687 mRNA sequence), R00761 (ye78b11.s1 Homo sapiens cDNA clone 123837 3'), T83434 (yd46b04.r1 Homo sapiens cDNA clone 111247 5'), T84080 (yd46b04.s1 Homo sapiens cDNA clone 111247 3'), and U00594 (Mustela vison unknown mRNA down regulated by TGF-beta, partial sequence). Based upon sequence similarity, kv10_8 proteins and each similar protein or peptide may share at least some activity. The 30 TopPredII computer program predicts a potential transmembrane domain within the kv10_8 protein sequence, centered around amino acids 35 to 45 of SEQ ID NO:120. The nucleotide sequence of kv10_8 indicates that it may contain one or more of the following repetitive elements: Alu, SVA.

Clone "LL89_3"

A polynucleotide of the present invention has been identified as clone "LL89_3". LL89_3 was isolated from a human adult thyroid cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of 5 the encoded protein. LL89_3 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "LL89_3 protein").

The nucleotide sequence of LL89_3 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the LL89_3 protein 10 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:122.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone LL89_3 should be approximately 900 bp.

The nucleotide sequence disclosed herein for LL89_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 15 FASTA search protocols. LL89_3 demonstrated at least some similarity with sequences identified as AL031010 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 422F24, complete sequence), H78002 (yu82h09.r1 Homo sapiens cDNA clone 240353 5'), and W90018 (zh72c08.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417614 3'). Based upon sequence similarity, LL89_3 proteins and each similar 20 protein or peptide may share at least some activity.

Clone "mc300_1"

A polynucleotide of the present invention has been identified as clone "mc300_1". mc300_1 was isolated from a human adult thyroid cDNA library and was identified as 25 encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mc300_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "mc300_1 protein").

The nucleotide sequence of mc300_1 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper 30 reading frame and the predicted amino acid sequence of the mc300_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mc300_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for mc300_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mc300_1 demonstrated at least some similarity with sequences identified as AA142942 (IMAGE 3p clone), AA315222 (EST187017 Colon carcinoma (HCC) 5 cell line Homo sapiens cDNA 5' end), AA142942 (zl43c04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 504678 3'), AI246503 (qn64a06.x1 NCI_CGAP_HN4 Homo sapiens cDNA clone IMAGE:1902994 3', mRNA sequence), D61461 (Human fetal brain cDNA 5'-end GEN-404B08), D79662 (Human aorta cDNA 5'-end GEN-300D05, mRNA sequence), H93575 (yv14h11.s1 Homo sapiens cDNA clone 242757 3'), T25928 10 (Human gene signature HUMGS08160; standard; cDNA to mRNA), and W93059 (zd93h06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357083 3'). Based upon sequence similarity, mc300_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of mc300_1 indicates that it may contain one or more Alu repetitive elements.

15

Clone "ml227_1"

A polynucleotide of the present invention has been identified as clone "ml227_1". ml227_1 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 20 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml227_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml227_1 protein").

The nucleotide sequence of ml227_1 as presently determined is reported in SEQ 25 ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml227_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml227_1 should be approximately 2700 bp.

30 The nucleotide sequence disclosed herein for ml227_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml227_1 demonstrated at least some similarity with sequences identified as AA857826 (oe88e05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1418720 3', mRNA sequence), F18464 (H.sapiens EST sequence (017-T4-16) from

skeletal muscle), H30845 (yo78d11.r1 Homo sapiens cDNA clone 184053 5'), T06839 (EST04728 Homo sapiens cDNA clone HFBDZ66), T19759 (Human gene signature HUMGS00834), T26021 (Human gene signature HUMGS08257; standard; cDNA to mRNA), and Z69043 (H.sapiens mRNA translocon-associated protein delta subunit precursor). The predicted amino acid sequence disclosed herein for ml227_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ml227_1 protein demonstrated at least some similarity to the sequence identified as Z69664 (K04D7.5 [Caenorhabditis elegans]). Based upon sequence similarity, ml227_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the ml227_1 protein sequence, centered around amino acids 465, 510, 560, 572, 595, and 615 of SEQ ID NO:126, respectively.

Clone "mm367_6"

15 A polynucleotide of the present invention has been identified as clone "mm367_6". mm367_6 was isolated from a human adult retina (WERI-Rb1 retinoblastoma line) cDNA library and was identified as encoding a protein. mm367_6 is a full-length clone, including the entire coding sequence of a protein (also referred to herein as "mm367_6 protein").

20 The nucleotide sequence of mm367_6 as presently determined is reported in SEQ ID NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mm367_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mm367_6 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for mm367_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mm367_6 demonstrated at least some similarity with sequences identified as AA114127 (zn65f02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563067 5'), AA127284 (zn91c12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565558 5'), AA173842 (zp30d01.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610945 5'), AF000364 (Homo sapiens heterogeneous nuclear ribonucleoprotein R mRNA, complete CDs), N31934 (yy22d10.s1 Homo sapiens cDNA clone 271987 3'), T24354 (Human gene signature HUMGS06385; standard; cDNA to

mRNA), U48271 (Dictyostelium discoideum UbpA deubiquitinase mRNA, complete CDs), W16579 (zb13g11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301988 5'), and W72461 (zd67f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345731 3'). The predicted amino acid sequence disclosed herein for mm367_6 was searched 5 against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mm367_6 protein demonstrated at least some similarity to sequences identified as AF000364 (heterogeneous nuclear ribonucleoprotein R [Homo sapiens]) and W26553 (Human heterogeneous nuclear ribonucleoprotein (hnRNP) A2). Based upon sequence similarity, mm367_6 proteins and each similar protein or peptide 10 may share at least some activity.

mm367_6 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 79 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15 Clone "mt124_3"

A polynucleotide of the present invention has been identified as clone "mt124_3". mt124_3 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mt124_3 is a full-length clone, including the entire coding sequence 20 of a novel protein (also referred to herein as "mt124_3 protein").

The nucleotide sequence of mt124_3 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mt124_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mt124_3 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for mt124_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mt124_3 demonstrated at least some similarity with sequences 30 identified as AA435386 (ve15h01.r1 Soares mouse NbMH Mus musculus cDNA clone 818257 5' similar to TR:E198756 E198756 PUTATIVE ORF), AI185116 (qe51g07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE 1742556 3' similar to TR Q92564 Q92564 MYELOBLAST KIAA0276 ; mRNA sequence), C03847 (Human Heart cDNA, clone 3NHC2256), N74186 (za76h03.s1 Homo sapiens cDNA clone 298517 3'),

T24234 (Human gene signature HUMGS06248; standard; cDNA to mRNA), W87997 (mf65b06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 419123 5'), and Z86062 (Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments). The predicted amino acid sequence disclosed herein for mt124_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mt124_3 protein demonstrated at least some similarity to sequences identified as AL024499 (H38K22.2 [Caenorhabditis elegans]) and D87466 (Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]).

10 Based upon sequence similarity, mt124_3 proteins and each similar protein or peptide may share at least some activity.

Clone "nf56_3"

A polynucleotide of the present invention has been identified as clone "nf56_3".

15 nf56_3 was isolated from a human adult brain (substantia nigra) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. nf56_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to

20 herein as "nf56_3 protein").

The nucleotide sequence of nf56_3 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the nf56_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 3 to 15

25 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the nf56_3 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone nf56_3 should be approximately 5000 bp.

The nucleotide sequence disclosed herein for nf56_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. nf56_3 demonstrated at least some similarity with sequences

identified as H08054 (yl86a09.s1 Homo sapiens cDNA clone 44915 3'), Q60495 (Human brain Expressed Sequence Tag EST02500; standard; cDNA), T25509 (Human gene signature HUMGS07678), W34534 (mc58h01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 352753 5'), and Z64987 (H.sapiens CpG island DNA genomic Mse1 fragment, clone 186b1, reverse read cpg186b1.rt1b). The predicted amino acid sequence disclosed herein for nf56_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted nf56_3 protein demonstrated at least some similarity to sequences identified as D86983 (similar to D.melanogaster peroxidasin (U11052) [Homo sapiens]), R25079 (Drosophila SLIT protein involved in axon pathway development), and X53959 (slit protein [Drosophila melanogaster]). Based upon sequence similarity, nf56_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the nf56_3 protein sequence, one centered around amino acid 514 and another around amino acid 628 of SEQ ID NO:132.

15

Clone "qy442_2"

A polynucleotide of the present invention has been identified as clone "qy442_2". qy442_2 was isolated from a human adult blood (promyelocytic leukemia HL-60 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qy442_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qy442_2 protein").

The nucleotide sequence of qy442_2 as presently determined is reported in SEQ ID NO:133, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qy442_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134. Amino acids 3 to 15 of SEQ ID NO:134 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qy442_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qy442_2 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for qy442_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qy442_2 demonstrated at least some similarity with sequences identified as AI081522 (on04e12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone 5 IMAGE:1555726 3' similar to contains Alu repetitive element; mRNA sequence) and AA449854 (zx37a06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788626 5'). Based upon sequence similarity, qy442_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the qy442_2 protein sequence, centered around amino acid 10 68 of SEQ ID NO:20. The nucleotide sequence of qy442_2 indicates that it may contain one or more Alu repetitive elements.

Clone "rj214_14"

A polynucleotide of the present invention has been identified as clone "rj214_14". rj214_14 was isolated from a human adult neural (neuroepithelioma HTB-10 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rj214_14 is a full-length clone, including the entire coding sequence of a secreted protein 20 (also referred to herein as "rj214_14 protein").

The nucleotide sequence of rj214_14 as presently determined is reported in SEQ ID NO:135, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rj214_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:136. 25 Amino acids 3 to 15 of SEQ ID NO:136 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rj214_14 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rj214_14 should be approximately 900 bp.

The nucleotide sequence disclosed herein for rj214_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rj214_14 demonstrated at least some similarity with sequences

identified as AA167035 (zp05c10.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595506 3' similar to TR:G563357 G563357 GENES RAS1, RLB1 AND RLC1; mRNA sequence), AA491109 (aa52d09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 824561 5' similar to TR G563357 G563357 GENES RAS1, RLB1 AND RLC1), and 5 AI189156 (qd04c02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1722722 3' similar to TR:O01437 O01437 SIMILAR TO DROSOPHILA RLC1 GENE PRODUCT; mRNA sequence). The predicted amino acid sequence disclosed herein for rj214_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted rj214_14 protein 10 demonstrated at least some similarity to sequences identified as U97016 (similar to drosophila Rlc1 gene product (NID g563361) and S. cerevisiae mitochondrial 60S ribosomal protein L4 (YML4) (NID g459259) [Caenorhabditis elegans]), and X73219 (Rlc1). Drosophila Rlc1 is a basic protein that is bound to the inner face of the cell membrane. Transcription mapping and nucleotide sequence analysis reveal that Rlc1 lies in the same 15 genomic region as Drosophila Ras1 and shows expression patterns that are similar to those of Ras1. It has been demonstrated (Ezer *et al.*, 1994, *Dev. Dyn.* 201(2): 179-190, which is incorporated by reference herein) that during embryogenesis Ras1 transcripts are restricted mainly to the embryonic central nervous system, suggesting that the Rlc1 gene product also may have a role in these nerve cells. Based upon sequence similarity, 20 rj214_14 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the rj214_14 protein sequence, centered around amino acid 32 of SEQ ID NO:136.

rj214_14 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in membrane fractions using SDS 25 polyacrylamide gel electrophoresis.

Clone "rk80_3"

A polynucleotide of the present invention has been identified as clone "rk80_3". rk80_3 was isolated from a human adult tumor (colorectal adenocarcinoma SW480 line) 30 cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. rk80_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "rk80_3 protein").

The nucleotide sequence of rk80_3 as presently determined is reported in SEQ ID NO:137, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the rk80_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:138. Amino acids 6 to 18 5 of SEQ ID NO:138 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the rk80_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone rk80_3 should be approximately 1096 bp.

The nucleotide sequence disclosed herein for rk80_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. rk80_3 demonstrated at least some similarity with sequences 15 identified as AA418955 (zw01c10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 768018 5', mRNA sequence), AB004061 (domestic pig mRNA for STAT2, complete CDs, a signal transducer and activator of transcription), C06368 (similar to none), and U38443 (Human clone JkA3 mRNA induced upon T-cell activation, 3' end). The predicted rk80_3 protein demonstrated at least some similarity to granulocyte-colony stimulating factor (G- 20 CSF) and interleukin-6 (IL-6). Hidden Markov model analysis has revealed the presence of an IL-6/G-CSF/mast cell growth factor (MGF) family signature at amino acids 69 to 181 of SEQ ID NO:138. This family of cytokines are glycoproteins of about 170 to 180 amino acid residues in size that contain four conserved cysteine residues involved in two disulfide bonds. rk80_3 appears to encode a novel cytokine in the IL-6/G-CSF family. 25 Based upon sequence similarity, rk80_3 proteins and each similar protein or peptide may share at least some activity.

rk80_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

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Clone "au36_42"

A polynucleotide of the present invention has been identified as clone "au36_42". au36_42 was isolated from a human adult testes cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of

the encoded protein. au36_42 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "au36_42 protein").

The nucleotide sequence of au36_42 as presently determined is reported in SEQ ID NO:139, and includes a poly(A) tail. What applicants presently believe to be the proper 5 reading frame and the predicted amino acid sequence of the au36_42 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:140.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone au36_42 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for au36_42 was searched against the 10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide sequence of au36_42 indicates that it may contain a L1ME repetitive element.

Clone "bo549_13"

15 A polynucleotide of the present invention has been identified as clone "bo549_13". bo549_13 was isolated from a human adult retina cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bo549_13 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bo549_13 protein").

20 The nucleotide sequence of bo549_13 as presently determined is reported in SEQ ID NO:141, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bo549_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:142. The region of SEQ ID NO:141 at nucleotides 518 and 519 may represent the border of an 25 alternatively spliced exon.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bo549_13 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for bo549_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and 30 FASTA search protocols. bo549_13 demonstrated at least some similarity with sequences identified as AI261562 (qz30c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE 2028394 3' similar to TR Q63061 Q63061 HYPOTHETICAL 4.7 KD PROTEIN; mRNA sequence) and J02649 (Rat stomach (H⁺,K⁺)-ATPase mRNA, complete cds). The predicted amino acid sequence disclosed herein for bo549_13 was searched against the GenPept and

GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bo549_13 protein demonstrated at least some similarity to sequences identified as J02649 (unknown protein [Rattus norvegicus]). Based upon sequence similarity, bo549_13 proteins and each similar protein or peptide may share at least some activity.

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Clone "da529_3"

A polynucleotide of the present invention has been identified as clone "da529_3". da529_3 was isolated from a human fetal placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was 10 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. da529_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "da529_3 protein").

The nucleotide sequence of da529_3 as presently determined is reported in SEQ 15 ID NO:143, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the da529_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:144. Amino acids 59 to 71 of SEQ ID NO:144 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 72. Due to the 20 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the da529_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone da529_3 should be approximately 1150 bp.

25 The nucleotide sequence disclosed herein for da529_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. da529_3 demonstrated at least some similarity with sequences identified as AI189911 (qd33e06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE 1725538 3' similar to TR O42204 O42204 PUTATIVE 30 TRANSMEMBRANE PROTEIN E3-16; mRNA sequence), T35254 (EST82005 Homo sapiens cDNA 5' end similar to None), U76253 (Mus musculus E25B protein mRNA, complete cds), V43619 (Human secreted protein 19 encoding DNA), W28608 (49b1 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA), and W41628 (mc47c10.r1 Soares mouse p3NMF19). The predicted amino acid sequence disclosed herein for

da529_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted da529_3 protein demonstrated at least some similarity to sequences identified as AF03895 (E25 protein [Homo sapiens]) and W63699 (Human secreted protein 19). Based upon sequence similarity, da529_3 proteins and each similar protein or peptide may share at least some activity.

Clone "dm365_3"

A polynucleotide of the present invention has been identified as clone "dm365_3". A cDNA clone was first isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate dm365_3 from a human fetal brain cDNA library. dm365_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dm365_3 protein").

The nucleotide sequence of dm365_3 as presently determined is reported in SEQ ID NO:145, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dm365_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:146. Amino acids 1 to 13 of SEQ ID NO:146 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Amino acids 40 to 52 of SEQ ID NO:146 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 53. Due to the hydrophobic nature of each of these predicted leader/signal sequences, each predicted leader/signal sequence is likely to act as a transmembrane domain should it not be separated from the remainder of the dm365_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dm365_3 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for dm365_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dm365_3 demonstrated at least some similarity with sequences identified as AC005533 (** SEQUENCING IN PROGRESS *** Homo sapiens clone DJ0794K21; HTGS phase 1, 22 unordered pieces), AI125562 (qd94d09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE 1737137 3', mRNA sequence), R02268 (ye85c10.r1

Homo sapiens cDNA clone 124530 5' similar to contains LTR5 repetitive element), and V90427 (EST clone DM365). Based upon sequence similarity, dm365_3 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dm365_3 indicates that it may contain repetitive sequences.

5 dm365_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 23 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "fa171_1"

10 A polynucleotide of the present invention has been identified as clone "fa171_1". fa171_1 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fa171_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "fa171_1 protein").

15 The nucleotide sequence of fa171_1 as presently determined is reported in SEQ ID NO:147, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fa171_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:148.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fa171_1 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for fa171_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fa171_1 demonstrated at least some similarity with sequences identified as AA446057 (zw66d04.r1 Soares testis NHT Homo sapiens cDNA clone 781159 25 5', mRNA sequence), AC002099 (**SEQUENCING IN PROGRESS *** Genomic sequence from Human 9q34; HTGS phase 1, 2 unordered pieces), AC002355 (**SEQUENCING IN PROGRESS *** Genomic sequence from Human 9q34; HTGS phase 1, 7 unordered pieces), and U10185 (Xenopus laevis XPMC2 protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for fa171_1 was searched against the GenPept and 30 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fa171_1 protein demonstrated at least some similarity to sequences identified as R67549 (Fruiting body inducing polypeptide) and U10185 (XPMC2 protein [Xenopus laevis]). XPMC2 is a Xenopus cDNA clone that can rescue several different yeast mitotic catastrophe mutants defective in Wee1 kinase function, and is a nuclear protein. Based

upon sequence similarity, fa171_1 proteins and each similar protein or peptide may share at least some activity.

Clone "lp572_2"

5 A polynucleotide of the present invention has been identified as clone "lp572_2". lp572_2 was isolated from a human adult blood (peripheral blood mononuclear cells treated with granulocyte-colony stimulating factor *in vivo*) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer
10 analysis of the amino acid sequence of the encoded protein. lp572_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lp572_2 protein").

The nucleotide sequence of lp572_2 as presently determined is reported in SEQ ID NO:149, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the lp572_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:150. Amino acids 79 to 91 of SEQ ID NO:150 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 92. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the lp572_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lp572_2 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for lp572_2 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. lp572_2 demonstrated at least some similarity with sequences identified as AA489012 (aa56a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 824908 3'), AA533633 (nf73b09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 925529, mRNA sequence), AC004686 (Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence), T18977 (g07030t Testis 1 Homo sapiens cDNA clone g07030 5' end),
30 T21490 (Human gene signature HUMGS02862), and W73324 (zd01h01.r1 Pancreatic Islet Homo sapiens cDNA clone 339409 5'). The predicted amino acid sequence disclosed herein for lp572_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted lp572_2 protein

demonstrated at least some similarity to sequences identified as AL03262 (predicted using Genefinder [Caenorhabditis elegans]). Based upon sequence similarity, lp572_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the 5 lp572_2 protein sequence, centered around amino acids 129, 263, 286, 326, and 378 of SEQ ID NO:150, respectively.

Clone "pe246_1"

A polynucleotide of the present invention has been identified as clone "pe246_1". 10 pe246_1 was isolated from a human adult blood (chronic myelogenous leukemia line K562) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe246_1 is a full-length clone, including the entire coding sequence 15 of a secreted protein (also referred to herein as "pe246_1 protein").

The nucleotide sequence of pe246_1 as presently determined is reported in SEQ ID NO:151, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe246_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:152. 20 Amino acids 193 to 205 of SEQ ID NO:152 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 206. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pe246_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe246_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for pe246_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe246_1 demonstrated at least some similarity with sequences 30 identified as AA234138 (zr51b06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 666899 5' similar to SW FCEB_HUMAN Q01362 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT), AA418443 (zv92e05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767264 5' similar to SW FCEB_RAT P13386 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT; mRNA sequence),

AC004584 (Homo sapiens chromosome 17, clone hRPC1107_A_17, complete sequence), M74509 (Human endogenous retrovirus type C oncovirus sequence), and V57903 (Hereditary haemochromatosis subregion from an HH affected individual). The predicted amino acid sequence disclosed herein for pe246_1 was searched against the GenPept and 5 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pe246_1 protein demonstrated at least some similarity to sequences identified as L35848 (IgE receptor beta subunit [Homo sapiens]), R05026 (Beta subunit of rat high affinity IgE receptor Fc(epsilon)RI), and R42341 (Subunit of the human IgE receptor). The first 359 nucleotides of SEQ ID NO:13 is similar in sequence to that of M74509 (Human 10 endogenous retrovirus type C oncovirus sequence) and also to several genomic sequences as a result. It appears that this region may be retroviral DNA that has been incorporated into the genome. Based upon sequence similarity, pe246_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the pe246_1 protein 15 sequence, centered around amino acids 86, 115, and 154 of SEQ ID NO:152, respectively.

Clone "qf122_3"

A polynucleotide of the present invention has been identified as clone "qf122_3". qf122_3 was isolated from a human adult bladder (carcinoma line 5637) cDNA library and 20 was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf122_3 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "qf122_3 protein").

The nucleotide sequence of qf122_3 as presently determined is reported in SEQ ID NO:153. What applicants presently believe to be the proper reading frame and the 25 predicted amino acid sequence of the qf122_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:154.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf122_3 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for qf122_3 was searched against the 30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf122_3 demonstrated at least some similarity with sequences identified as AA206909 (zq80d10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 647923 5' similar to SW YYAF_BACSU P37518 HYPOTHETICAL 40.1 KD GTP-BINDING PROTEIN IN RPSF-SPO0J INTERGENIC REGION; mRNA sequence),

AA237053 (zs01c01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 683904 5' similar to SW YBN5_YEAST P38219 HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION), AA775776 (ad14e03.s1 Soares NbHFB Homo sapiens cDNA clone 878236 3' similar to TR P91917 P91917 W08E3.3; mRNA sequence), AL021878 (Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2; contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS), and N32932 (yy10a02.s1 Homo sapiens cDNA clone 270794 3' similar to SW:YBN5_YEAST P38219 HYPOTHETICAL 44.2 KD PROTEIN IN SCO2-MRF1 INTERGENIC REGION). The predicted amino acid sequence disclosed herein for qf122_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qf122_3 protein demonstrated at least some similarity to sequences identified as W48670 (Staphylococcus aureus gbpA protein), Z92773 (W08E3.3 [Caenorhabditis elegans]), and Z92773 (predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW P38219); cDNA EST EMBL D64516 comes from this gene). Based upon sequence similarity, qf122_3 proteins and each similar protein or peptide may share at least some activity. Analysis of protein motifs in SEQ ID NO:154 predicts an ATP/GTP-binding site motif A (P-loop) around amino acid 29 of SEQ ID NO:154.

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Clone "qv538_1"

A polynucleotide of the present invention has been identified as clone "qv538_1". qv538_1 was isolated from a human adult testes (embryonal carcinoma NT2D1 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qv538_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qv538_1 protein").

The nucleotide sequence of qv538_1 as presently determined is reported in SEQ ID NO:155, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qv538_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:156. Amino acids 8 to 20 of SEQ ID NO:156 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the

hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qv538_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone 5 qv538_1 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for qv538_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qv538_1 demonstrated at least some similarity with sequences identified as W44974 (zc22e11.r1 Soares senescent fibroblasts NbHSF Homo sapiens 10 cDNA clone 323084 5' similar to SW:FKB2_YEAST P32472 FK506-BINDING PROTEIN PRECURSOR; mRNA sequence), and Z62799 (H.sapiens CpG island DNA genomic Mse1 fragment, clone 73c8, reverse read cpg73c8.rt1a). The predicted amino acid sequence disclosed herein for qv538_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qv538_1 protein 15 demonstrated at least some similarity to sequences identified as AF04025 (FK506-binding protein [Mus musculus]) and W88556 (Secreted protein encoded by gene 23 clone HSQEO84). FK506-binding protein (or "FKBP") is the major high-affinity binding protein, in vertebrates, for the immunosuppressive drug FK506 (used to aid in organ transplantation acceptance among other indications). It exhibits peptidyl-prolyl cis-trans 20 isomerase activity (PPIase or rotamase). PPIase is an enzyme that accelerates protein folding by catalyzing the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. Based upon sequence similarity, qv538_1 proteins and each similar protein or peptide may share at least some activity. Analysis of protein motifs in SEQ ID NO:156 25 detects an endoplasmic reticulum targeting sequence around amino acid 208. Hidden Markov Model analysis detects an EF-hand calcium-binding domain at amino acids 183 to 211 of SEQ ID NO:156 (also found by motif analysis) and a FKBP-type peptidyl-prolyl cis-trans isomerase signatures/profile at amino acids 38 to 132 of SEQ ID NO:156. The nucleotide sequence of qv538_1 indicates that it may contain an Alu repetitive element.

qv538_1 protein was expressed in a COS cell expression system, and an expressed 30 protein band of approximately 24 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "ys20_1"

A polynucleotide of the present invention has been identified as clone "ys20_1". ys20_1 was isolated from a human adult thymus cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the 5 amino acid sequence of the encoded protein. ys20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ys20_1 protein").

The nucleotide sequence of ys20_1 as presently determined is reported in SEQ ID NO:157, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ys20_1 protein corresponding 10 to the foregoing nucleotide sequence is reported in SEQ ID NO:158. Amino acids 41 to 53 of SEQ ID NO:158 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Amino acids 121 to 133 of SEQ ID NO:158 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 134. Due to the hydrophobic nature of each 15 of these predicted leader/signal sequences, each predicted leader/signal sequence is likely to act as a transmembrane domain should it not be separated from the remainder of the ys20_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ys20_1 should be approximately 2229 bp.

20 The nucleotide sequence disclosed herein for ys20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ys20_1 demonstrated at least some similarity with sequences identified as B76357 (RPCI11-15B19.TV RPCI11 Homo sapiens genomic clone R-15B19, genomic survey sequence). Based upon sequence similarity, ys20_1 proteins and each 25 similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the ys20_1 protein sequence, centered around amino acid 205 of SEQ ID NO:158. The nucleotide sequence of ys20_1 indicates that it may contain one or more mammalian transposon-like long terminal repeat elements, such as MCT1b/c.

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Clone "as180_1"

A polynucleotide of the present invention has been identified as clone "as180_1". as180_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. as180_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "as180_1 protein").

5 The nucleotide sequence of as180_1 as presently determined is reported in SEQ ID NO:159. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the as180_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:160. Amino acids 168 to 180 of SEQ ID NO:160 are a predicted leader/signal sequence, with the predicted mature amino acid 10 sequence beginning at amino acid 181. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the as180_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone as180_1 should be approximately 3580 bp.

15 The nucleotide sequence disclosed herein for as180_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. as180_1 demonstrated at least some similarity with sequences identified as AB018279 (Homo sapiens mRNA for KIAA0736 protein, complete cds), S47919 (p87 = transporter-like protein [cattle, mRNA]), V89585 (EST clone CR618), and 20 W28902 (53d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence). The predicted amino acid sequence disclosed herein for as180_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted as180_1 protein demonstrated at least some similarity to sequences identified as AB018279 (KIAA0736 protein [Homo sapiens]), 25 L05435 (synaptic vesicle protein 2 [Rattus norvegicus]), S47919 (p87 [Bos sp.]), and W64538 (Human liver cell clone HP01293 protein). Synaptic vesicle protein 2 (SV2) is a membrane glycoprotein specifically localized to secretory vesicles in neurons and endocrine cells (Bajjali, S.M. *et al.*, 1992, *Science* Aug 28; **257**(5074):1271-1273, which is incorporated by reference herein). Based upon sequence similarity, as180_1 proteins and 30 each similar protein or peptide may share at least some activity. Analysis of amino acid motifs detected a sugar-transport protein signature around amino acid 264 of SEQ ID NO:160, and hidden Markov Model analysis detected a sugar-transporter amino acid profile from amino acid 153 to amino acid 741 of SEQ ID NO:160. The TopPredII

computer program predicts twelve potential transmembrane domains within the as180_1 protein sequence, centered around amino acids 181, 205, 248, 270, 308, 344, 432, 458, 605, 638, 654, and 710 of SEQ ID NO:160, respectively.

5 Deposit of Clones

Clones co62_12, lo311_8, ns197_1, pj193_5, pj317_2, pt332_1, qc297_15, qg596_12, and rb649_3 were deposited on July 29, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98825, from 10 which each clone comprising a particular polynucleotide is obtainable.

Clones ca106_19xx, ci52_2, md124_16, pk366_7, pl741_5, pp314_19, pv35_1, pw337_6, rd610_1, and rd810_6 were deposited on August 11, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession 15 number ATCC 98835, from which each clone comprising a particular polynucleotide is obtainable.

Clones cf85_1, dd504_18, np26_3, pm412_12, pm421_3, pv6_1, qs14_3, qy338_9, rc58_1, and rd232_5 were deposited on August 27, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an 20 original deposit under the Budapest Treaty and were given the accession number ATCC 98850, from which each clone comprising a particular polynucleotide is obtainable.

Clones ck213_12, pg195_1, pw460_5, qa136_1, qy1261_2, and rd432_4 were deposited on October 8, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under 25 the Budapest Treaty and were given the accession number ATCC 98918, from which each clone comprising a particular polynucleotide is obtainable.

Clones rb789_14, yd137_1, yd218_1, ye11_1, ye72_1, ye78_1, ye90_1, yi62_1, yk78_1, yk251_1, and yt14_1 were deposited on December 15, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 30 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207004, from which each clone comprising a particular polynucleotide is obtainable.

Clones bf157_16, bk343_2, cd205_2, cw1292_8, cw1475_2, dd428_4, dh1073_12, dw78_1, fh116_11, fy356_14, and iw66_1 were deposited on February 4, 1999 with the

American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207088, from which each clone comprising a particular polynucleotide is obtainable.

5 Clones kh13_4, ko258_4, kv10_8, LL89_3, mc300_1, ml227_1, mm367_6, mt124_3, nf56_3, qy442_2, rj214_1, and rk80_3 were deposited on February 4, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207089, from which each clone comprising a particular 10 polynucleotide is obtainable.

Clones au36_42, bo549_13, da529_3, dm365_3, fa171_1, lp572_2, pe246_1, qf122_3, qv538_1, and ys20_1 were deposited on April 2, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 15 207187, from which each clone comprising a particular polynucleotide is obtainable.

Clone as180_1 was deposited on August 11, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 20 XXXXXX, from which the as180_1 clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

25 Each clone has been transfected into separate bacterial cells (*E. coli*) in the above composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively, or in the case of clone qs14_3, 30 in the pCMV Sport2 vector (Life Technologies, Inc., Rockville, MD 20850, U.S.A.) depicted in Figure 2. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and

insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

5 Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is 10 known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
	co62_12	SEQ ID NO:161
	lo311_8	SEQ ID NO:162
	ns197_1	SEQ ID NO:163
	pj193_5	SEQ ID NO:164
20	pj317_2	SEQ ID NO:165
	pt332_1	SEQ ID NO:166
	qc297_15	SEQ ID NO:167
	qg596_12	SEQ ID NO:168
	rb649_3	SEQ ID NO:169
25	ca106_19x	SEQ ID NO:170
	ci52_2	SEQ ID NO:171
	md124_16	SEQ ID NO:172
	pk366_7	SEQ ID NO:173
	pl741_5	SEQ ID NO:174
30	pp314_19	SEQ ID NO:175
	pv35_1	SEQ ID NO:176
	pw337_6	SEQ ID NO:177
	rd610_1	SEQ ID NO:178
	rd810_6	SEQ ID NO:179

	cf85_1	SEQ ID NO:180
	dd504_18	SEQ ID NO:181
	np26_3	SEQ ID NO:182
	pm412_12	SEQ ID NO:183
5	pm421_3	SEQ ID NO:184
	pv6_1	SEQ ID NO:185
	qs14_3	SEQ ID NO:186
	qy338_9	SEQ ID NO:187
	rc58_1	SEQ ID NO:188
10	rd232_5	SEQ ID NO:189
	ck213_12	SEQ ID NO:190
	pg195_1	SEQ ID NO:191
	pw460_5	SEQ ID NO:192
	qa136_1	SEQ ID NO:193
15	qy1261_2	SEQ ID NO:194
	rd432_4	SEQ ID NO:195
	rb789_14	SEQ ID NO:196
	yd137_1	SEQ ID NO:197
	ye11_1	SEQ ID NO:198
20	ye72_1	SEQ ID NO:199
	ye78_1	SEQ ID NO:200
	ye90_1	SEQ ID NO:201
	yk251_1	SEQ ID NO:202
	yt14_1	SEQ ID NO:203
25	bf157_16	SEQ ID NO:204
	bk343_2	SEQ ID NO:205
	cd205_2	SEQ ID NO:206
	cw1292_8	SEQ ID NO:207
	cw1475_2	SEQ ID NO:208
30	dd428_4	SEQ ID NO:209
	dh1073_12	SEQ ID NO:210
	dw78_1	SEQ ID NO:211
	fh116_11	SEQ ID NO:212
	fy356_14	SEQ ID NO:213

	iw66_1	SEQ ID NO:214
	kh13_4	SEQ ID NO:215
	ko258_4	SEQ ID NO:216
	kv10_8	SEQ ID NO:217
5	LL89_3	SEQ ID NO:218
	mc300_1	SEQ ID NO:219
	ml227_1	SEQ ID NO:220
	mm367_6	SEQ ID NO:221
	mt124_3	SEQ ID NO:222
10	nf56_3	SEQ ID NO:223
	qy442_2	SEQ ID NO:224
	rij214_14	SEQ ID NO:225
	rk80_3	SEQ ID NO:226
	au36_42	SEQ ID NO:227
15	bo549_13	SEQ ID NO:228
	da529_3	SEQ ID NO:229
	dm365_3	SEQ ID NO:230
	fa171_1	SEQ ID NO:231
	lp572_2	SEQ ID NO:232
20	pe246_1	SEQ ID NO:233
	qf122_3	SEQ ID NO:234
	qv538_1	SEQ ID NO:235
	ys20_1	SEQ ID NO:236
	as180_1	SEQ ID NO:237

25

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoaramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

(b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e-6 dpm/pmole.

5 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the 10 dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

15 Standard colony hybridization procedures should then be used to transfer the 10 colonies to nitrocellulose filters and lyse, denature and bake them.

20 The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μ g/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at 25 a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The 30 filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, *Bio/Technology* 10, 773-778 (1992) and in R.S. McDowell, *et al.*, *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that

has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately 5 labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences 10 disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology 15 Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense 20 polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). The desired change in gene 25 expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* 391 (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* 95 (26): 15502-15507; and Sharp, 1999, *Genes Dev.* 13 (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have 30 multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are

also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through 5 deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, 10 preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for 15 the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part 20 or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of 25 transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmsmbrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most 30 preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are

proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

5 In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX 10 platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely 15 used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length 20 one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue 25 penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one 30 through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps.

The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or 5 polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence 10 identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from 15 the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, 20 *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species 25 (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides 30 or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90%

identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and

5 screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly

10 stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T _F *; 1xSSC	T _F *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T _J *; 4xSSC	T _J *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T _R *; 4xSSC	T _R *; 4xSSC

[‡]: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM Na₂HPO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

30 ^{*}T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,

5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined 20 herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the 25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or 5 enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, 10 e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

15 The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column 20 containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

25 Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and 30 Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to 5 provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which 10 are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by 15 virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

20 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, 25 insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, 30 insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

5 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies
10 or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express
15 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare
20 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out"
known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for
25 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those
30 described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine 5 levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the 10 protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent 15 grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to 20 Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein 25 or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention 30 can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is 5 evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro assays for Mouse Lymphocyte Function* 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., *J. Immunol.* 137:3494-3500, 1986; 15 Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include; without limitation, those described in: *Polyclonal T cell stimulation*, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and *Measurement of mouse and human Interferon γ* , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic 25 cells include, without limitation, those described in: *Measurement of Human and Murine Interleukin 2 and Interleukin 4*, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; 30 *Measurement of mouse and human interleukin 6* - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; *Measurement of human Interleukin 11* - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, 5 proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and 10 their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

15 Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., 20 in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a 25 protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

30 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present

5 invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by 10 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is 15 distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing 20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated 25 through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the 30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as 10 described in Lenschow *et al.*, *Science* 257:789-792 (1992) and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15 Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.

20 Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from 25 the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and 30 murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B 5 lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in* 10 *vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfet them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a 15 costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present 20 invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The 25 transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary 30 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2

microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995;

10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

15 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993;

20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

25

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet 5 disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without 10 limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

15 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, 20 proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among 25 others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and 30 Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

5

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, 10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as 15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal 20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue 25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in 30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The 5 compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal 10 tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and 15 peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, 20 Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the 25 invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for 30 generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, 5 and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

15 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

20 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present 25 invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- 30 β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity 10 (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide 15 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it 20 can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured 25 by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion 30 include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting 10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

20 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, 25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant 30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static 5 conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

10 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the 15 inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic 20 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to 30 tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this 5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells 10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas 15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed 20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the 25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block 30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in 5 ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without 10 limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or 15 prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by 20 inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

25 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ 30 or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

5 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another

10 material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a

15 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the

20 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other

25 agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor,

30 thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.

When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should 5 contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

10 The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician 15 will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 20 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is 25 contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

30 Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of 5 antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the 10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing 15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be 20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide 25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, *J. Amer. Chem. Soc.* 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, *FEBS Lett.* 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful 30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

- 5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably
- 10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the
- 15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical
- 20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other

- 25 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions 5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of 10 carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to 15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in 20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to 25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of 30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such 5 polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present 10 invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.